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FROM THE SAME PATIENTcDNA PREPARED
FROM BREAST TUMOR

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(57) Abstract

Compositions and methods for the detection and therapy of breast cancer are disclosed. The compounds provided include nucleotide sequences that are preferentially expressed in breast tumor tissue, as well as polypeptides encoded by such nucleotide sequences. Vaccines and pharmaceutical compositions comprising such compounds are also provided and may be used, for example, for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of antibodies, which are useful for diagnosing and monitoring the progression of breast cancer in a patient.

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COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER

TECHNICAL FIELD

The present invention relates generally to the detection and therapy of breast cancer. The invention is more specifically related to nucleotide sequences that are preferentially expressed in breast tumor tissue and to polypeptides encoded by such nucleotide sequences. The nucleotide sequences and polypeptides may be used in vaccines and pharmaceutical compositions for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of breast cancer in a patient.

BACKGROUND OF THE INVENTION

Breast cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and treatment of the disease, breast cancer remains the second leading cause of cancer-related deaths in women, affecting more than 180,000 women in the United States each year. For women in North America, the life-time odds of getting breast cancer are now one in eight.

No vaccine or other universally successful method for the prevention or treatment of breast cancer is currently available. Management of the disease currently relies on a combination of early diagnosis (through routine breast screening procedures) and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular breast cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. See, e.g., Porter-Jordan and Lippman, *Breast Cancer* 8:73-100 (1994). However, the use of established markers often leads to a result that is difficult to interpret, and the high mortality observed in

breast cancer patients indicates that improvements are needed in the treatment, diagnosis and prevention of the disease.

Accordingly, there is a need in the art for improved methods for therapy and diagnosis of breast cancer. The present invention fulfills these needs and further
5 provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the subject invention provides compositions and methods for the diagnosis and therapy of breast cancer. In one aspect, isolated polynucleotides are provided, comprising (a) a nucleotide sequence preferentially expressed in breast cancer
10 tissue, relative to normal tissue; (b) a variant of such a sequence, as defined below; or (c) a nucleotide sequence encoding an epitope of a polypeptide encoded by at least one of the above sequences. In one embodiment, the isolated polynucleotide comprises a human endogenous retroviral sequence recited in SEQ ID NO:1. In other embodiments, the isolated polynucleotide comprises a sequence recited in any one of SEQ ID NO: 3-
15 26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317.

In related embodiments, the isolated polynucleotide encodes an epitope of
20 a polypeptide, wherein the polypeptide is encoded by a nucleotide sequence that: (a) hybridizes to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 under stringent
25 conditions; and (b) is at least 80% identical to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317.

In another embodiment, the present invention provides an isolated polynucleotide encoding an epitope of a polypeptide, the polypeptide being encoded by: (a) a nucleotide sequence transcribed from the sequence of SEQ ID NO: 141; or (b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained. Isolated DNA and RNA molecules comprising a nucleotide sequence complementary to a polynucleotide as described above are also provided.

In related aspects, the present invention provides recombinant expression vectors comprising a polynucleotide as described above and host cells transformed or transfected with such expression vectors.

In further aspects, polypeptides comprising an amino acid sequence encoded by a polynucleotide as described above, and monoclonal antibodies that bind to such polypeptides are provided. In certain embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 299, 300, 304-306, 308 and 315, and variants thereof as defined below.

In yet another aspect, methods are provided for determining the presence of breast cancer in a patient. In one embodiment, the method comprises detecting, within a biological sample, a polypeptide as described above. In another embodiment, the method comprises detecting, within a biological sample, an RNA molecule encoding a polypeptide as described above. In yet another embodiment, the method comprises (a) intradermally injecting a patient with a polypeptide as described above; and (b) detecting an immune response on the patient's skin and therefrom detecting the presence of breast cancer in the patient. In further embodiments, the present invention provides methods for determining the presence of breast cancer in a patient as described above wherein the polypeptide is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In a related aspect, diagnostic kits useful in the determination of breast cancer are provided. The diagnostic kits generally comprise either one or more monoclonal antibodies as described above, or one or more monoclonal antibodies that bind to a polypeptide encoded by a nucleotide sequence selected from the group consisting of sequences provided in SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and a detection reagent.

Diagnostic kits are also provided that comprise a first polymerase chain reaction primer and a second polymerase chain reaction primer, at least one of the primers being specific for a polynucleotide described herein. In one embodiment, at least one of the primers comprises at least about 10 contiguous nucleotides of a polynucleotide as described above, or a polynucleotide encoding a polypeptide encoded by a sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

Within another related aspect, the diagnostic kit comprises at least one oligonucleotide probe, the probe being specific for a polynucleotide described herein. In one embodiment, the probe comprises at least about 15 contiguous nucleotides of a polynucleotide as described above, or a polynucleotide selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

In another related aspect, the present invention provides methods for monitoring the progression of breast cancer in a patient. In one embodiment, the method comprises: (a) detecting an amount, in a biological sample, of a polypeptide as described above at a first point in time; (b) repeating step (a) at a subsequent point in time; and (c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient. In another embodiment, the method comprises (a) detecting an amount, within a biological sample, of an RNA molecule encoding a polypeptide as described above at a first point in time; (b) repeating

step (a) at a subsequent point in time; and (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient. In yet other embodiments, the present invention provides methods for monitoring the progression of breast cancer in a patient as described above wherein the polypeptide is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In still other aspects, pharmaceutical compositions, which comprise a polypeptide as described above in combination with a physiologically acceptable carrier, and vaccines, which comprise a polypeptide as described above in combination with an immunostimulant or adjuvant, are provided. In yet other aspects, the present invention provides pharmaceutical compositions and vaccines comprising a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In related aspects, the present invention provides methods for inhibiting the development of breast cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as described above.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the differential display PCR products, separated by gel electrophoresis, obtained from cDNA prepared from normal breast tissue (lanes 1 and 2) and from cDNA prepared from breast tumor tissue from the same patient (lanes 3 and 4). The arrow indicates the band corresponding to B18Ag1.

Figure 2 is a northern blot comparing the level of B18Ag1 mRNA in breast tumor tissue (lane 1) with the level in normal breast tissue.

Figure 3 shows the level of B18Ag1 mRNA in breast tumor tissue compared to that in various normal and non-breast tumor tissues as determined by RNase protection assays.

Figure 4 is a genomic clone map showing the location of additional retroviral sequences obtained from ends of XbaI restriction digests (provided in SEQ ID NO:3 - SEQ ID NO:10) relative to B18Ag1.

Figures 5A and 5B show the sequencing strategy, genomic organization and predicted open reading frame for the retroviral element containing B18Ag1.

Figure 6 shows the nucleotide sequence of the representative breast tumor-specific cDNA B18Ag1.

Figure 7 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag1.

Figure 8 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag2.

Figure 9 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag2a.

Figure 10 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1b.

Figure 11 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1a.

Figure 12 shows the nucleotide sequence of the representative breast tumor-specific cDNA B11Ag1.

Figure 13 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3c.

Figure 14 shows the nucleotide sequence of the representative breast tumor-specific cDNA B9CG1.

Figure 15 shows the nucleotide sequence of the representative breast tumor-specific cDNA B9CG3.

Figure 16 shows the nucleotide sequence of the representative breast tumor-specific cDNA B2CA2.

Figure 17 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA1.

5 Figure 18 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA2.

Figure 19 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3.

10 Figure 20 shows the nucleotide sequence of the representative breast tumor-specific cDNA B4CA1.

Figure 21A depicts RT-PCR analysis of breast tumor genes in breast tumor tissues (lanes 1-8) and normal breast tissues (lanes 9-13) and H₂O (lane 14).

15 Figure 21B depicts RT-PCR analysis of breast tumor genes in prostate tumors (lane 1, 2), colon tumors (lane 3), lung tumor (lane 4), normal prostate (lane 5), normal colon (lane 6), normal kidney (lane 7), normal liver (lane 8), normal lung (lane 9), normal ovary (lanes 10, 18), normal pancreases (lanes 11, 12), normal skeletal muscle (lane 13), normal skin (lane 14), normal stomach (lane 15), normal testes (lane 16), normal small intestine (lane 17), HBL-100 (lane 19), MCF-12A (lane 20), breast tumors (lanes 21-23), H₂O (lane 24), and colon tumor (lane 25).

20 Figure 22 shows the recognition of a B11Ag1 peptide (referred to as B11-8) by an anti-B11-8 CTL line.

Figure 23 shows the recognition of a cell line transduced with the antigen B11Ag1 by the B11-8 specific clone A1.

25 Figure 24 shows recognition of a lung adenocarcinoma line (LT-140-22) and a breast adenocarcinoma line (CAMA-1) by the B11-8 specific clone A1.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the diagnosis, monitoring and therapy of breast cancer. The compositions described herein include polypeptides, polynucleotides and antibodies.

Polypeptides of the present invention generally comprise at least a portion of a protein that is expressed at a greater level in human breast tumor tissue than in normal breast tissue (*i.e.*, the level of RNA encoding the polypeptide is at least 2-fold higher in tumor tissue). Such polypeptides are referred to herein as breast tumor-specific polypeptides, and cDNA molecules encoding such polypeptides are referred to as breast tumor-specific cDNAs. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of a polypeptide as described above, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or fragments thereof, that are capable of binding to a portion of a polypeptide as described above. Antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies.

Polypeptides within the scope of this invention include, but are not limited to, polypeptides (and epitopes thereof) encoded by a human endogenous retroviral sequence, such as the sequence designated B18Ag1 (Figure 5 and SEQ ID NO:1). Also within the scope of the present invention are polypeptides encoded by other sequences within the retroviral genome containing B18Ag1 (SEQ ID NO: 141). Such sequences include, but are not limited to, the sequences recited in SEQ ID NO:3 - SEQ ID NO:10. B18Ag1 has homology to the *gag* p30 gene of the endogenous human retroviral element S71, as described in Werner et al., *Virology* 174:225-238 (1990) and also shows homology to about thirty other retroviral *gag* genes. As discussed in more detail below, the present invention also includes a number of additional breast tumor-specific polypeptides, such as those encoded by the nucleotide sequences recited in SEQ ID NO: 11-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317.

As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins containing the sequences recited herein. A

polypeptide comprising an epitope of a protein containing a sequence as described herein may consist entirely of the epitope, or may contain additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may (but need not) possess immunogenic or antigenic properties.

5 An "epitope," as used herein is a portion of a polypeptide that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Epitopes may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides derived
10 from the native polypeptide for the ability to react with antigen-specific antisera and/or T-cell lines or clones. An epitope of a polypeptide is a portion that reacts with such antisera and/or T-cells at a level that is similar to the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such screens may generally be performed using methods well known to those of ordinary skill in the art,
15 such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. B-cell and T-cell epitopes may also be predicted via computer analysis. Polypeptides comprising an epitope of a polypeptide that is preferentially expressed in a tumor tissue (with or without additional amino acid sequence) are within the scope of the present invention.

20 The term "polynucleotide(s)," as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule contains
25 introns and corresponds to a DNA molecule in a generally one-to-one manner. An mRNA molecule corresponds to an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes
30 all such operable anti-sense fragments.

The compositions and methods of the present invention also encompass variants of the above polypeptides and polynucleotides.

A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the antigenic properties of the polypeptide are retained. In a preferred embodiment, variant polypeptides differ from an identified sequence by substitution, deletion or addition of five amino acids or fewer. Such variants may generally be identified by modifying one of the above polypeptide sequences, and evaluating the antigenic properties of the modified polypeptide using, for example, the representative procedures described herein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described below) to the identified polypeptides.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or

additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity (determined as described below) to the recited sequence.

The breast tumor antigens provided by the present invention include variants that are encoded by DNA sequences which are substantially homologous to one or more of the DNA sequences specifically recited herein. "Substantial homology," as used herein, refers to DNA sequences that are capable of hybridizing under moderately stringent conditions. Suitable moderately stringent conditions include prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5X SSC, overnight or, in the event of cross-species homology, at 45°C with 0.5X SSC; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. Such hybridizing DNA sequences are also within the scope of this invention, as are nucleotide sequences that, due to code degeneracy, encode an immunogenic polypeptide that is encoded by a hybridizing DNA sequence.

Two nucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acid residues in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment

schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) Fast and sensitive multiple sequence alignments on a microcomputer *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) Optimal alignments in linear space *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) The neighbor joining method. A new method for reconstructing phylogenetic trees *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) Rapid similarity searches of nucleic acid and protein data banks *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity. In general, polynucleotides encoding all or a portion of the polypeptides described herein may be prepared using any of several techniques. For example, cDNA molecules encoding such polypeptides may be cloned on the basis of the breast tumor-specific expression of the corresponding mRNAs, using differential display PCR. This technique compares the amplified products from RNA template prepared from normal and breast tumor tissue. cDNA may

be prepared by reverse transcription of RNA using a (dT)₁₂AG primer. Following amplification of the cDNA using a random primer, a band corresponding to an amplified product specific to the tumor RNA may be cut out from a silver stained gel and subcloned into a suitable vector (e.g., the T-vector, Novagen, Madison, WI).

- 5 Polynucleotides encoding all or a portion of the breast tumor-specific polypeptides disclosed herein may be amplified from cDNA prepared as described above using the random primers shown in SEQ ID NO.:87-125.

Alternatively, a polynucleotide encoding a polypeptide as described herein (or a portion thereof) may be amplified from human genomic DNA, or from breast
10 tumor cDNA, via polymerase chain reaction. For this approach, B18Ag1 sequence-specific primers may be designed based on the sequence provided in SEQ ID NO:1, and may be purchased or synthesized. One suitable primer pair for amplification from breast tumor cDNA is (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO:126) and (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO:127). An amplified portion of
15 B18Ag1 may then be used to isolate the full length gene from a human genomic DNA library or from a breast tumor cDNA library, using well known techniques, such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY (1989). Other sequences within the retroviral genome of which B18Ag1 is a part may be similarly prepared by screening
20 human genomic libraries using B18Ag1-specific sequences as probes. Nucleotides translated into protein from the retroviral genome shown in SEQ ID NO: 141 may then be determined by cloning the corresponding cDNAs, predicting the open reading frames and cloning the appropriate cDNAs into a vector containing a viral promoter, such as T7. The resulting constructs can be employed in a translation reaction, using techniques
25 known to those of skill in the art, to identify nucleotide sequences which result in expressed protein. Similarly, primers specific for the remaining breast tumor-specific polypeptides described herein may be designed based on the nucleotide sequences provided in SEQ ID NO:11-86, 142-298, 301-303, 307, 313, 314, 316 and 317.

Recombinant polypeptides encoded by the DNA sequences described
30 above may be readily prepared from the DNA sequences. For example, supernatants

from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps
5 can be employed to further purify a recombinant polypeptide.

In general, any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide that
10 encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO.

Such techniques may also be used to prepare polypeptides comprising epitopes or variants of the native polypeptides. For example, variants of a native
15 polypeptide may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis, and sections of the DNA sequence may be removed to permit preparation of truncated polypeptides. Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to
20 those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146 (1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as
25 Perkin Elmer/Applied BioSystems Division,, Foster City, CA, and may be operated according to the manufacturer's instructions.

In specific embodiments, polypeptides of the present invention encompass amino acid sequences encoded by a polynucleotide having a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198,
30 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255,

257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317, and variants of such polypeptides. Polypeptides within the scope of the present invention also include polypeptides (and epitopes thereof) encoded by DNA sequences that hybridize to a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 under stringent conditions, wherein the DNA sequences are at least 80% identical in overall sequence to a recited sequence and wherein RNA corresponding to the nucleotide sequence is expressed at a greater level in human breast tumor tissue than in normal breast tissue. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2 X SSC, 0.1% SDS at 65°C. Polynucleotides according to the present invention include molecules that encode any of the above polypeptides.

In another aspect of the present invention, antibodies are provided. Such antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519 (1976), and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Antibodies may be used, for example, in methods for detecting breast cancer in a patient. Such methods involve using an antibody to detect the presence or absence of a breast tumor-specific polypeptide as described herein in a suitable biological sample. As used herein, suitable biological samples include tumor or normal tissue biopsy, mastectomy, blood, lymph node, serum or urine samples, or other tissue, homogenate, or extract thereof obtained from a patient.

There are a variety of assay formats known to those of ordinary skill in the art for using an antibody to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, the assay may be performed in a Western blot format, wherein a protein preparation from the biological sample is submitted to gel electrophoresis, transferred to a suitable membrane and allowed to react with the antibody. The presence of the antibody on the membrane may then be detected using a suitable detection reagent, as described below.

In another embodiment, the assay involves the use of antibody immobilized on a solid support to bind to the polypeptide and remove it from the remainder of the sample. The bound polypeptide may then be detected using a second antibody or reagent that contains a reporter group. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized antibody after incubation of the antibody with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the antibody is indicative of the reactivity of the sample with the immobilized antibody, and as a result, indicative of the concentration of polypeptide in the sample.

The solid support may be any material known to those of ordinary skill in the art to which the antibody may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose filter or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The antibody may be immobilized on the solid support using a variety of techniques known to those in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a

well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the antibody, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of antibody ranging from about 10 ng to about 1 μ g, and preferably about 100-200 ng, is sufficient to immobilize an adequate amount of polypeptide.

Covalent attachment of antibody to a solid support may also generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the antibody. For example, the antibody may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook (1991) at A12-A13).

In certain embodiments, the assay for detection of polypeptide in a sample is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the biological sample, such that the polypeptide within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation

time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with breast cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will
5 recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody,
10 which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

15 The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed
20 for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter
25 groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of breast cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value established from non-tumor
30 tissue. In one preferred embodiment, the cut-off value is the average mean signal

obtained when the immobilized antibody is incubated with samples from patients without breast cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value may be considered positive for breast cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver
5 Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, p. 106-7 (Little Brown and Co., 1985). Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot
10 that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample
15 generating a signal that is higher than the cut-off value determined by this method is considered positive for breast cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, the polypeptide within the sample bind to the immobilized
20 antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample
25 migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of breast cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general,
30 the amount of antibody immobilized on the membrane is selected to generate a visually

discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 1 μ g. Such tests can typically be performed with a very small amount of biological sample.

The presence or absence of breast cancer in a patient may also be determined by evaluating the level of mRNA encoding a breast tumor-specific polypeptide as described herein within the biological sample (e.g., a biopsy, mastectomy and/or blood sample from a patient) relative to a predetermined cut-off value. Such an evaluation may be achieved using any of a variety of methods known to those of ordinary skill in the art such as, for example, *in situ* hybridization and amplification by polymerase chain reaction.

For example, polymerase chain reaction may be used to amplify sequences from cDNA prepared from RNA that is isolated from one of the above biological samples. Sequence-specific primers for use in such amplification may be designed based on the sequences provided in any one of SEQ ID NO: 1, 11-86, 142-298 301-303, 307, 313, 314, 316 and 317, and may be purchased or synthesized. In the case of B18Ag1, as noted herein, one suitable primer pair is B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO:126) and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO:127). The PCR reaction products may then be separated by gel electrophoresis and visualized according to methods well known to those of ordinary skill in the art. Amplification is typically performed on samples obtained from matched pairs of tissue (tumor and non-tumor tissue from the same individual) or from unmatched pairs of tissue (tumor and non-tumor tissue from different individuals). The amplification reaction is preferably performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the tumor sample as compared to the same dilution of the non-tumor sample is considered positive.

As used herein, the term "primer/probe specific for a polynucleotide" means an oligonucleotide sequence that has at least about 80% identity, preferably at least about 90% and more preferably at least about 95%, identity to the polynucleotide in question, or an oligonucleotide sequence that is anti-sense to a sequence that has at least about 80% identity, preferably at least about 90% and more preferably at least about 95%, identity to the polynucleotide in question. Primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the polymerase chain reaction primers comprise at least about 10 contiguous nucleotides of a polynucleotide that encodes one of the polypeptides disclosed herein or that is anti-sense to a sequence that encodes one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a polynucleotide that encodes one of the polypeptides disclosed herein or that is anti-sense to a sequence that encodes one of the polypeptides disclosed herein. Techniques for both PCR based assays and *in situ* hybridization assays are well known in the art.

Conventional RT-PCR protocols using agarose and ethidium bromide staining, while important in defining gene specificity, do not lend themselves to diagnostic kit development because of the time and effort required in making them quantitative (i.e., construction of saturation and/or titration curves), and their sample throughput. This problem is overcome by the development of procedures such as real time RT-PCR which allows for assays to be performed in single tubes, and in turn can be modified for use in 96 well plate formats. Instrumentation to perform such methodologies are available from Perkin Elmer/Applied Biosystems Division. Alternatively, other high throughput assays using labeled probes (e.g., digoxigenin) in combination with labeled (e.g., enzyme fluorescent, radioactive) antibodies to such probes can also be used in the development of 96 well plate assays.

In yet another method for determining the presence or absence of breast cancer in a patient, one or more of the breast tumor-specific polypeptides described may be used in a skin test. As used herein, a "skin test" is any assay performed directly on a patient in which a delayed-type hypersensitivity (DTH) reaction (such as swelling,

reddening or dermatitis) is measured following intradermal injection of one or more polypeptides as described above. Such injection may be achieved using any suitable device sufficient to contact the polypeptide or polypeptides with dermal cells of the patient, such as a tuberculin syringe or 1 mL syringe. Preferably, the reaction is measured at least 48 hours after injection, more preferably 48-72 hours.

The DTH reaction is a cell-mediated immune response, which is greater in patients that have been exposed previously to a test antigen (*i.e.*, an immunogenic portion of a polypeptide employed, or a variant thereof). The response may be measured visually, using a ruler. In general, a response that is greater than about 0.5 cm in diameter, preferably greater than about 5.0 cm in diameter, is a positive response, indicative of breast cancer.

The breast tumor-specific polypeptides described herein are preferably formulated, for use in a skin test, as pharmaceutical compositions containing at least one polypeptide and a physiologically acceptable carrier, such as water, saline, alcohol, or a buffer. Such compositions typically contain one or more of the above polypeptides in an amount ranging from about 1 μ g to 100 μ g, preferably from about 10 μ g to 50 μ g in a volume of 0.1 mL. Preferably, the carrier employed in such pharmaceutical compositions is a saline solution with appropriate preservatives, such as phenol and/or Tween 80TM.

In other aspects of the present invention, the progression and/or response to treatment of a breast cancer may be monitored by performing any of the above assays over a period of time, and evaluating the change in the level of the response (*i.e.*, the amount of polypeptide or mRNA detected or, in the case of a skin test, the extent of the immune response detected). For example, the assays may be performed every month to every other month for a period of 1 to 2 years. In general, breast cancer is progressing in those patients in whom the level of the response increases over time. In contrast, breast cancer is not progressing when the signal detected either remains constant or decreases with time.

In further aspects of the present invention, the compounds described herein may be used for the immunotherapy of breast cancer. In these aspects, the

compounds (which may be polypeptides, antibodies or polynucleotides) are preferably incorporated into pharmaceutical compositions or vaccines. Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds in combination with an immunostimulant, such as an adjuvant or a liposome (into which the compound is incorporated). An immunostimulant may be any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (e.g., polylactic galactide) and liposomes (into which the compound is incorporated; see e.g., Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

Alternatively, a vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. In such vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749 (1993), and reviewed by

Cohen, *Science* 259:1691-1692 (1993). The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the

induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Corixa Corporation (Seattle, WA; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555 and WO 99/33488. Immunostimulatory DNA sequences are also described, for example, by Sato et al., *Science* 273:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Other preferred adjuvants include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (e.g., SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Ribi ImmunoChem Research Inc., Hamilton, MT), RC-529 (Ribi ImmunoChem Research Inc., Hamilton, MT) and Aminoalkyl glucosaminide 4-phosphates (AGPs).

Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immunostimulant and a suitable carrier or excipient. The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology (*see, e.g.*, Coombes et al., *Vaccine* 14:1429-1438, 1996) and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane.

Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), as well as polyacrylate, latex, starch, cellulose and dextran. Other delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA

haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (see Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible

intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fcγ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a polypeptide of the present invention (or portion or other variant thereof) such that the polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Vaccines and pharmaceutical compositions may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are preferably hermetically sealed to preserve sterility of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a vaccine or pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier

immediately prior to use.

The above pharmaceutical compositions and vaccines may be used, for example, for the therapy of breast cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with breast cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of breast cancer or to treat a patient afflicted with breast cancer. In a preferred embodiment, the compounds are administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs. To prevent or slow the development of breast cancer, a pharmaceutical composition or vaccine comprising one or more polypeptides as described herein may be administered to a patient. Alternatively, naked DNA or plasmid or viral vector encoding the polypeptide may be administered. For treating a patient with breast cancer, the pharmaceutical composition or vaccine may comprise one or more polypeptides, antibodies or polynucleotides complementary to DNA encoding a polypeptide as described herein (e.g., antisense RNA or antisense deoxyribonucleotide oligonucleotides).

Routes and frequency of administration, as well as dosage, will vary from individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered for a 52-week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (e.g., more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical

compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 µg to 5 mg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

5 Polypeptides disclosed herein may also be employed in adoptive immunotherapy for the treatment of cancer. Adoptive immunotherapy may be broadly classified into either active or passive immunotherapy. In active immunotherapy, treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (for
10 example, tumor vaccines, bacterial adjuvants, and/or cytokines).

In passive immunotherapy, treatment involves the delivery of biologic reagents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T lymphocytes (for
15 example, CD8+ cytotoxic T-lymphocyte, CD4+ T-helper, tumor-infiltrating lymphocytes), killer cells (Natural Killer cells, lymphokine-activated killer cells), B cells, or antigen presenting cells (such as dendritic cells and macrophages) expressing the disclosed antigens. The polypeptides disclosed herein may also be used to generate antibodies or anti-idiotypic antibodies (as in U.S. Patent No. 4,918,164), for passive
20 immunotherapy.

The predominant method of procuring adequate numbers of T-cells for adoptive immunotherapy is to grow immune T-cells *in vitro*. Culture conditions for expanding single antigen-specific T-cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. These *in vitro* culture conditions
25 typically utilize intermittent stimulation with antigen, often in the presence of cytokines, such as IL-2, and non-dividing feeder cells. As noted above, the immunoreactive polypeptides described herein may be used to rapidly expand antigen-specific T cell cultures in order to generate sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage or B-cells, may be pulsed with
30 immunoreactive polypeptides or transfected with a polynucleotide sequence(s), using

standard techniques well known in the art. For cultured T-cells to be effective in therapy, the cultured T-cells must be able to grow and distribute widely and to survive long term *in vivo*. Studies have demonstrated that cultured T-cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation
5 with antigen supplemented with IL-2 (see, for example, Cheever et al. *Ibid*).

The polypeptides disclosed herein may also be employed to generate and/or isolate tumor-reactive T-cells, which can then be administered to the patient. In one technique, antigen-specific T-cell lines may be generated by *in vivo* immunization with short peptides corresponding to immunogenic portions of the disclosed
10 polypeptides. The resulting antigen specific CD8+ CTL clones may be isolated from the patient, expanded using standard tissue culture techniques, and returned to the patient.

Alternatively, peptides corresponding to immunogenic portions of the polypeptides may be employed to generate tumor reactive T cell subsets by selective *in vitro* stimulation and expansion of autologous T cells to provide antigen-specific T cells
15 which may be subsequently transferred to the patient as described, for example, by Chang et al. (*Crit. Rev. Oncol. Hematol.*, 22(3), 213, 1996).

In another embodiment, syngeneic or autologous dendritic cells may be pulsed with peptides corresponding to at least an immunogenic portion of a polypeptide disclosed herein. The resulting antigen-specific dendritic cells may either be transferred
20 into a patient, or employed to stimulate T cells to provide antigen-specific T cells which may, in turn, be administered to a patient. The use of peptide-pulsed dendritic cells to generate antigen-specific T cells and the subsequent use of such antigen-specific T cells to eradicate tumors in a murine model has been demonstrated by Cheever et al. ("Therapy With Cultured T Cells: Principles Revisited," *Immunological Reviews*,
25 157:177, 1997).

Additionally vectors expressing the disclosed polynucleotides may be introduced into stem cells taken from the patient and clonally propagated *in vitro* for autologous transplant back into the same patient. In one embodiment, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a
30 commercially available cell separation system, such as CellPro Incorporated's (Bothell,

WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

PREPARATION OF BREAST TUMOR-SPECIFIC cDNAS USING DIFFERENTIAL DISPLAY RT-PCR

This Example illustrates the preparation of cDNA molecules encoding breast tumor-specific polypeptides using a differential display screen.

A. Preparation of B18Ag1 cDNA and Characterization of mRNA Expression

Tissue samples were prepared from breast tumor and normal tissue of a patient with breast cancer that was confirmed by pathology after removal from the patient. Normal RNA and tumor RNA was extracted from the samples and mRNA was isolated and converted into cDNA using a (dT)₁₂AG (SEQ ID NO:130) anchored 3' primer. Differential display PCR was then executed using a randomly chosen primer (CTTCAACCTC) (SEQ ID NO:103). Amplification conditions were standard buffer containing 1.5 mM MgCl₂, 20 pmol of primer, 500 pmol dNTP, and 1 unit of *Taq* DNA polymerase (Perkin-Elmer, Branchburg, NJ). Forty cycles of amplification were performed using 94°C denaturation for 30 seconds, 42°C annealing for 1 minute, and 72°C extension for 30 seconds. An RNA fingerprint containing 76 amplified products was

obtained. Although the RNA fingerprint of breast tumor tissue was over 98% identical to that of the normal breast tissue, a band was repeatedly observed to be specific to the RNA fingerprint pattern of the tumor. This band was cut out of a silver stained gel, subcloned into the T-vector (Novagen, Madison, WI) and sequenced.

5 The sequence of the cDNA, referred to as B18Ag1, is provided in SEQ ID NO:1. A database search of GENBANK and EMBL revealed that the B18Ag1 fragment initially cloned is 77% identical to the endogenous human retroviral element S71, which is a truncated retroviral element homologous to the Simian Sarcoma Virus (SSV). S71 contains an incomplete *gag* gene, a portion of the *pol* gene and an LTR-like structure at
10 the 3' terminus (*see* Werner et al., *Virology* 174:225-238 (1990)). B18Ag1 is also 64% identical to SSV in the region corresponding to the P30 (*gag*) locus. B18Ag1 contains three separate and incomplete reading frames covering a region which shares considerable homology to a wide variety of *gag* proteins of retroviruses which infect mammals. In addition, the homology to S71 is not just within the *gag* gene, but spans
15 several kb of sequence including an LTR.

B18Ag1-specific PCR primers were synthesized using computer analysis guidelines. RT-PCR amplification (94°C, 30 seconds; 60°C → 42°C, 30 seconds; 72°C, 30 seconds for 40 cycles) confirmed that B18Ag1 represents an actual mRNA sequence present at relatively high levels in the patient's breast tumor tissue. The primers used in
20 amplification were B18Ag1-1 (CTG CCT GAG CCA CAA ATG) (SEQ ID NO:128) and B18Ag1-4 (CCG GAG GAG GAA GCT AGA GGA ATA) (SEQ ID NO:129) at a 3.5 mM magnesium concentration and a pH of 8.5, and B18Ag1-2 (ATG GCT ATT TTC GGG GCC TGA CA) (SEQ ID NO:126) and B18Ag1-3 (CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO:127) at 2 mM magnesium at pH 9.5. The same experiments
25 showed exceedingly low to nonexistent levels of expression in this patient's normal breast tissue (*see* Figure 1). RT-PCR experiments were then used to show that B18Ag1 mRNA is present in nine other breast tumor samples (from Brazilian and American patients) but absent in, or at exceedingly low levels in, the normal breast tissue corresponding to each cancer patient. RT-PCR analysis has also shown that the B18Ag1
30 transcript is not present in various normal tissues (including lymph node, myocardium

and liver) and present at relatively low levels in PBMC and lung tissue. The presence of B18Ag1 mRNA in breast tumor samples, and its absence from normal breast tissue, has been confirmed by Northern blot analysis, as shown in Figure 2.

The differential expression of B18Ag1 in breast tumor tissue was also confirmed by RNase protection assays. Figure 3 shows the level of B18Ag1 mRNA in various tissue types as determined in four different RNase protection assays. Lanes 1-12 represent various normal breast tissue samples, lanes 13-25 represent various breast tumor samples; lanes 26-27 represent normal prostate samples; lanes 28-29 represent prostate tumor samples; lanes 30-32 represent colon tumor samples; lane 33 represents normal aorta; lane 34 represents normal small intestine; lane 35 represents normal skin, lane 36 represents normal lymph node; lane 37 represents normal ovary; lane 38 represents normal liver; lane 39 represents normal skeletal muscle; lane 40 represents a first normal stomach sample, lane 41 represents a second normal stomach sample; lane 42 represents a normal lung; lane 43 represents normal kidney; and lane 44 represents normal pancreas. Interexperimental comparison was facilitated by including a positive control RNA of known β -actin message abundance in each assay and normalizing the results of the different assays with respect to this positive control.

RT-PCR and Southern Blot analysis has shown the B18Ag1 locus to be present in human genomic DNA as a single copy endogenous retroviral element. A genomic clone of approximately 12-18 kb was isolated using the initial B18Ag1 sequence as a probe. Four additional subclones were also isolated by XbaI digestion. Additional retroviral sequences obtained from the ends of the XbaI digests of these clones (located as shown in Figure 4) are shown as SEQ ID NO:3 - SEQ ID NO:10, where SEQ ID NO:3 shows the location of the sequence labeled 10 in Figure 4, SEQ ID NO:4 shows the location of the sequence labeled 11-29, SEQ ID NO:5 shows the location of the sequence labeled 3, SEQ ID NO:6 shows the location of the sequence labeled 6, SEQ ID NO:7 shows the location of the sequence labeled 12, SEQ ID NO:8 shows the location of the sequence labeled 13, SEQ ID NO:9 shows the location of the sequence labeled 14 and SEQ ID NO:10 shows the location of the sequence labeled 11-22.

Subsequent studies demonstrated that the 12-18 kb genomic clone contains a retroviral element of about 7.75 kb, as shown in Figures 5A and 5B. The sequence of this retroviral element is shown in SEQ ID NO: 141. The numbered line at the top of Figure 5A represents the sense strand sequence of the retroviral genomic clone.

5 The box below this line shows the position of selected restriction sites. The arrows depict the different overlapping clones used to sequence the retroviral element. The direction of the arrow shows whether the single-pass subclone sequence corresponded to the sense or anti-sense strand. Figure 5B is a schematic diagram of the retroviral element containing B18Ag1 depicting the organization of viral genes within the element. The

10 open boxes correspond to predicted reading frames, starting with a methionine, found throughout the element. Each of the six likely reading frames is shown, as indicated to the left of the boxes, with frames 1-3 corresponding to those found on the sense strand.

Using the cDNA of SEQ ID NO:1 as a probe, a longer cDNA was obtained (SEQ ID NO:227) which contains minor nucleotide differences (less than 1%)

15 compared to the genomic sequence shown in SEQ ID NO:141.

B. Preparation of cDNA Molecules Encoding Other Breast Tumor-Specific Polypeptides

Normal RNA and tumor RNA was prepared and mRNA was isolated and converted into cDNA using a (dT)₁₂AG anchored 3' primer, as described above.

20 Differential display PCR was then executed using the randomly chosen primers of SEQ ID NO: 87-125. Amplification conditions were as noted above, and bands observed to be specific to the RNA fingerprint pattern of the tumor were cut out of a silver stained gel, subcloned into either the T-vector (Novagen, Madison, WI) or the pCRII vector (Invitrogen, San Diego, CA) and sequenced. The sequences are provided in SEQ ID

25 NO:11 - SEQ ID NO:86. Of the 79 sequences isolated, 67 were found to be novel (SEQ ID NO:11-26 and 28-77) (*see also* Figures 6-20).

An extended DNA sequence (SEQ ID NO: 290) for the antigen B15Ag1 (originally identified partial sequence provided in SEQ ID NO: 27) was obtained in further studies. Comparison of the sequence of SEQ ID NO: 290 with those in the gene

30 bank as described above, revealed homology to the known human β -A activin gene.

Further studies led to the isolation of the full-length cDNA sequence for the antigen B21GT2 (also referred to as B311D; originally identified partial cDNA sequence provided in SEQ ID NO: 56). The full-length sequence is provided in SEQ ID NO: 307, with the corresponding amino acid sequence being provided in SEQ ID NO: 308.

5 Further studies led to the isolation of a splice variant of B311D. The B311D clone of SEQ ID NO: 316 was sequenced and a XhoI/NotI fragment from this clone was gel purified and 32P-cDTP labeled by random priming for use as a probe for further screening to obtain additional B311D gene sequence. Two fractions of a human breast tumor cDNA bacterial library were screened using standard techniques. One of the

10 clones isolated in this manner yielded additional sequence which includes a poly A+ tail. The determined cDNA sequence of this clone (referred to as B311D_BT1_1A) is provided in SEQ ID NO: 317. The sequences of SEQ ID NO: 316 and 317 were found to share identity over a 464 bp region, with the sequences diverging near the poly A+ sequence of SEQ ID NO: 317.

15 Subsequent studies identified an additional 146 sequences (SEQ ID NOS:142-289), of which 115 appeared to be novel (SEQ ID NOS:142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291). To the best of the inventors' knowledge none of the previously

20 identified sequences have heretofore been shown to be expressed at a greater level in human breast tumor tissue than in normal breast tissue.

In further studies, several different splice forms of the antigen B11Ag1 (also referred to as B305D) were isolated, with each of the various splice forms containing slightly different versions of the B11Ag1 coding frame. Splice junction

25 sequences define individual exons which, in various patterns and arrangements, make up the various splice forms. Primers were designed to examine the expression pattern of each of the exons using RT-PCR as described below. Each exon was found to show the same expression pattern as the original B11Ag1 clone, with expression being breast tumor-, normal prostate- and normal testis-specific. The determined cDNA sequences

30 for the isolated protein coding exons are provided in SEQ ID NO: 292-298, respectively.

The predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292 and 298 are provided in SEQ ID NO: 299 and 300. Additional studies using rapid amplification of cDNA ends (RACE), a 5' specific primer to one of the splice forms of B11Ag1 provided above and a breast adenocarcinoma, led to the isolation of three additional, related, splice forms referred to as isoforms B11C-15, B11C-8 and B11C-9,16. The determined cDNA sequences for these isoforms are provided in SEQ ID NO: 301-303, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 304-306.

In subsequent studies on B305D isoform A (cDNA sequence provided in SEQ ID NO: 292), the cDNA sequence (provided in SEQ ID NO: 313) was found to contain an additional guanine residue at position 884, leading to a frameshift in the open reading frame. The determined DNA sequence of this ORF is provided in SEQ ID NO: 314. This frameshift generates a protein sequence (provided in SEQ ID NO: 315) of 293 amino acids that contains the C-terminal domain common to the other isoforms of B305D but that differs in the N-terminal region.

EXAMPLE 2

PREPARATION OF B18AG1 DNA FROM HUMAN GENOMIC DNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human genomic DNA.

B18Ag1 DNA may be prepared from 250 ng human genomic DNA using 20 pmol of B18Ag1 specific primers, 500 pmol dNTPS and 1 unit of *Taq* DNA polymerase (Perkin Elmer, Branchburg, NJ) using the following amplification parameters: 94°C for 30 seconds denaturing, 30 seconds 60°C to 42°C touchdown annealing in 2°C increments every two cycles and 72°C extension for 30 seconds. The last increment (a 42°C annealing temperature) should cycle 25 times. Primers were selected using computer analysis. Primers synthesized were B18Ag1-1, B18Ag1-2, B18Ag1-3, and B18Ag1-4. Primer pairs that may be used are 1+3, 1+4, 2+3, and 2+4.

Following gel electrophoresis, the band corresponding to B18Ag1 DNA may be excised and cloned into a suitable vector.

EXAMPLE 3

5 PREPARATION OF B18Ag1 DNA FROM BREAST TUMOR cDNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human breast tumor cDNA.

First strand cDNA is synthesized from RNA prepared from human breast
10 tumor tissue in a reaction mixture containing 500 ng poly A+ RNA, 200 pmol of the primer (T)₁₂AG (*i.e.*, TTT TTT TTT TTT AG) (SEQ ID NO: 130), 1X first strand reverse transcriptase buffer, 6.7 mM DTT, 500 mmol dNTPs, and 1 unit AMV or MMLV reverse transcriptase (from any supplier, such as Gibco-BRL (Grand Island, NY)) in a final volume of 30 μ l. After first strand synthesis, the cDNA is diluted approximately 25
15 fold and 1 μ l is used for amplification as described in Example 2. While some primer pairs can result in a heterogeneous population of transcripts, the primers B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO: 126) and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO: 127) yield a single 151 bp amplification product.

20

EXAMPLE 4

IDENTIFICATION OF B-CELL AND T-CELL EPITOPES OF B18Ag1

This Example illustrates the identification of B18Ag1 epitopes.

25 The B18Ag1 sequence can be screened using a variety of computer algorithms. To determine B-cell epitopes, the sequence can be screened for hydrophobicity and hydrophilicity values using the method of Hopp, *Prog. Clin. Biol. Res.* 172B:367-77 (1985) or, alternatively, Cease et al., *J. Exp. Med.* 164:1779-84 (1986) or Spouge et al., *J. Immunol.* 138:204-12 (1987). Additional Class II MHC (antibody or
30 B-cell) epitopes can be predicted using programs such as AMPHI (*e.g.*, Margalit et al., *J.*

Immunol. 138:2213 (1987)) or the methods of Rothbard and Taylor (e.g., *EMBO J.* 7:93 (1988)).

Once peptides (15-20 amino acids long) are identified using these techniques, individual peptides can be synthesized using automated peptide synthesis equipment (available from manufacturers such as Perkin Elmer/Applied Biosystems Division, Foster City, CA) and techniques such as Merrifield synthesis. Following synthesis, the peptides can be used to screen sera harvested from either normal or breast cancer patients to determine whether patients with breast cancer possess antibodies reactive with the peptides. Presence of such antibodies in breast cancer patient would confirm the immunogenicity of the specific B-cell epitope in question. The peptides can also be tested for their ability to generate a serologic or humoral immune response in animals (mice, rats, rabbits, chimps etc.) following immunization *in vivo*. Generation of a peptide-specific antiserum following such immunization further confirms the immunogenicity of the specific B-cell epitope in question.

To identify T-cell epitopes, the B18Ag1 sequence can be screened using different computer algorithms which are useful in identifying 8-10 amino acid motifs within the B18Ag1 sequence which are capable of binding to HLA Class I MHC molecules. (see, e.g., Rammensee et al., *Immunogenetics* 41:178-228 (1995)). Following synthesis such peptides can be tested for their ability to bind to class I MHC using standard binding assays (e.g., Sette et al., *J. Immunol.* 153:5586-92 (1994)) and more importantly can be tested for their ability to generate antigen reactive cytotoxic T-cells following *in vitro* stimulation of patient or normal peripheral mononuclear cells using, for example, the methods of Bakker et al., *Cancer Res.* 55:5330-34 (1995); Visseren et al., *J. Immunol.* 154:3991-98 (1995); Kawakami et al., *J. Immunol.* 154:3961-68 (1995); and Kast et al., *J. Immunol.* 152:3904-12 (1994). Successful *in vitro* generation of T-cells capable of killing autologous (bearing the same Class I MHC molecules) tumor cells following *in vitro* peptide stimulation further confirms the immunogenicity of the B18Ag1 antigen. Furthermore, such peptides may be used to generate murine peptide and B18Ag1 reactive cytotoxic T-cells following *in vivo* immunization in mice rendered

transgenic for expression of a particular human MHC Class I haplotype (Vitiello et al., *J. Exp. Med.* 173:1007-15 (1991)).

A representative list of predicted B18Ag1 B-cell and T-cell epitopes, broken down according to predicted HLA Class I MHC binding antigen, is shown below:

5

Predicted Th Motifs (B-cell epitopes) (SEQ ID NOS.: 131-133)

SSGGRTFDDFHRYLLVGI
QGAAQKPINLSKXIEVVQGHDE
SPGVFLEHLQEAYRIYTPFDLSA

10

Predicted HLA A2.1 Motifs (T-cell epitopes) (SEQ ID NOS.: 134-140)

YLLVGIQGA
GAAQKPINL
NLSKXIEVV
EVVQGHDES
HLQEAYRIY
NLAQVAQAA
FVAQAAPDS

15

20

EXAMPLE 5

IDENTIFICATION OF T-CELL EPITOPES OF B11Ag1

This Example illustrates the identification of B11Ag1 (also referred to as B305D) epitopes. Four peptides, referred to as B11-8, B11-1, B11-5 and B11-12 (SEQ ID NO: 309-312, respectfully) were derived from the B11Ag1 gene.

25

Human CD8 T cells were primed *in vitro* to the peptide B11-8 using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8 T cell cultures were tested for their ability to recognize the B11-8 peptide or a negative control peptide, presented by the B-LCL line, JY. Briefly, T cells were incubated with autologous monocytes in the presence of 10 ug/ml peptide, 10 ng/ml IL-7 and 10 ug/ml IL-2, and assayed for their ability to

30

specifically lyse target cells in a standard 51-Cr release assay. As shown in Fig. 22, the bulk culture line demonstrated strong recognition of the B11-8 peptide with weaker recognition of the peptide B11-1.

A clone from this CTL line was isolated following rapid expansion using the monoclonal antibody OKT3 and human IL-2. As shown in Fig. 23, this clone (referred to as A1), in addition to being able to recognize specific peptide, recognized JY LCL transduced with the B11Ag1 gene. This data demonstrates that B11-8 is a naturally processed epitope of the B11Ag1 gene. In addition these T cells were further found to recognize and lyse, in an HLA-A2 restricted manner, an established tumor cell line naturally expressing B11Ag1 (Fig. 24). The T cells strongly recognize a lung adenocarcinoma (LT-140-22) naturally expressing B11Ag1 transduced with HLA-A2, as well as an A2+ breast carcinoma (CAMA-1) transduced with B11Ag1, but not untransduced lines or another negative tumor line (SW620).

These data clearly demonstrate that these human T cells recognize not only B11-specific peptides but also transduced cells, as well as naturally expressing tumor lines.

CTL lines raised against the antigens B11-5 and B11-12, using the procedures described above, were found to recognize corresponding peptide-coated targets.

Example 6

CHARACTERIZATION OF BREAST TUMOR GENES DISCOVERED BY
DIFFERENTIAL DISPLAY PCR

5 The specificity and sensitivity of the breast tumor genes discovered by differential display PCR were determined using RT-PCR. This procedure enabled the rapid evaluation of breast tumor gene mRNA expression semiquantitatively without using large amounts of RNA. Using gene specific primers, mRNA expression levels in a variety of tissues were examined, including 8 breast tumors, 5 normal breasts, 2 prostate
10 tumors, 2 colon tumors, 1 lung tumor, and 14 other normal adult human tissues, including normal prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach and testes.

 To ensure the semiquantitative nature of the RT-PCR, β -actin was used as internal control for each of the tissues examined. Serial dilutions of the first strand
15 cDNAs were prepared and RT-PCR assays performed using β -actin specific primers. A dilution was then selected that enabled the linear range amplification of β -actin template, and which was sensitive enough to reflect the difference in the initial copy number. Using this condition, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and
20 by assuring a negative result when using first strand cDNA that was prepared without adding reverse transcriptase.

 Using gene specific primers, the mRNA expression levels were determined in a variety of tissues. To date, 38 genes have been successfully examined by RT-PCR, five of which exhibit good specificity and sensitivity for breast tumors
25 (B15AG-1, B31GA1b, B38GA2a, B11A1a and B18AG1a). Figures 21A and 21B depict the results for three of these genes: B15AG-1 (SEQ ID NO:27), B31GA1b (SEQ ID NO:148) and B38GA2a (SEQ ID NO. 157). Table I summarizes the expression level of all the genes tested in normal breast tissue and breast tumors, and also in other tissues.

TABLE I

Percentage of Breast Cancer Antigens that are Expressed in Various Tissues

5	Breast Tissues	Over-expressed in Breast Tumors	84%
		Equally Expressed in Normals and Tumor	16%
10	Other Tissues	Over-expressed in Breast Tumors but not in any Normal Tissues	9%
		Over-expressed in Breast Tumors but Expressed in Some Normal Tissues	30%
15		Over-expressed in Breast Tumors but Equally Expressed in All Other Tissues	61%

20 From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

CLAIMS

1. An isolated polypeptide, comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
- (a) sequences recited in SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317;
 - (b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and
 - (c) complements of sequences of (a) or (b).
2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences.
3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NOs: 299, 300, 304-306, 308 and 315.
4. An isolated polynucleotide encoding at least 15 amino acid

residues of a protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing sequences.

10

5. An isolated polynucleotide encoding a protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing sequences.

6. An isolated polynucleotide, comprising a sequence recited in any one of SEQ ID Nos: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317.

7. An isolated polynucleotide, comprising a sequence that hybridizes to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector, comprising a polynucleotide according to
5 any one of claims claim 4-8.

10. A host cell transformed or transfected with an expression vector according to claim 9.

10 11. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276,
15 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences.

12. A fusion protein, comprising at least one polypeptide according to claim 1.

20

13. A fusion protein according to claim 12, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

25

14. A fusion protein according to claim 12, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

15. A fusion protein according to claim 12, wherein the fusion
30 protein comprises an affinity tag.

16. An isolated polynucleotide encoding a fusion protein according to claim 12.

17. A pharmaceutical composition, comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- (d) a fusion protein according to claim 12; and
- (e) a polynucleotide according to claim 16.

18. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- (d) a fusion protein according to claim 12; and
- (e) a polynucleotide according to claim 16.

19. A vaccine according to claim 18, wherein the immunostimulant is an adjuvant.

20. A vaccine according to any claim 18, wherein the immunostimulant induces a predominantly Type I response.

21. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 17.

22. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to

claim 18.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a
5 pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

10 25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-
15 298, 301-303, 307, 313, 314, 316 and 317;

(b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and

(c) complements of sequences of (i) or (ii);
20 in combination with an immunostimulant.

26. A vaccine according to claim 25, wherein the immunostimulant is an adjuvant.

25 27. A vaccine according to claim 25, wherein the immunostimulant induces a predominantly Type I response.

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

30

29. A method for inhibiting the development of a cancer in a patient,

comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

5 (a) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

(b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and

10 (c) complements of sequences encoded by a polynucleotide recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

and thereby inhibiting the development of a cancer in the patient.

15 30. A method according to claim 29, wherein the antigen-presenting cell is a dendritic cell.

31. A method according to any one of claims 21, 22 and 29, wherein the cancer is breast cancer.

20

32. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

25 (i) polynucleotides recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317; and

(ii) complements of the foregoing polynucleotides;

wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the antigen from the sample.

30

33. A method according to claim 32, wherein the biological sample is

blood or a fraction thereof.

34. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 32.

35. A method for stimulating and/or expanding T cells specific for a protein, comprising contacting T cells with at least one component selected from the group consisting of:

- (a) polypeptides comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
- (i) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;
 - (ii) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and
 - (iii) complements of sequences of (i) or (ii);
- (b) polynucleotides encoding a polypeptide of (a); and
- (c) antigen presenting cells that express a polypeptide of (a);
- under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

36. An isolated T cell population, comprising T cells prepared according to the method of claim 35.

37. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 36.

30

38. A method for inhibiting the development of a cancer in a patient,

comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

5 (i) polypeptides comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(1) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

10 (2) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and

(3) complements of sequences of (1) or (2);

(ii) polynucleotides encoding a polypeptide of (i); and

15 (iii) antigen presenting cells that expresses a polypeptide of (i);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

20

39. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

25 (i) polypeptides comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(1) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

30

(2) sequences that hybridize to a sequence recited in

any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and

- (3) complements of sequences of (1) or (2);
 - (ii) polynucleotides encoding a polypeptide of (i); and
 - (iii) antigen presenting cells that express a polypeptide
- 5 of (i);

such that T cells proliferate;

- (b) cloning at least one proliferated cell to provide cloned T cells;
- and
- (c) administering to the patient an effective amount of the cloned
- 10 T cells, and thereby inhibiting the development of a cancer in the patient.

40. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

- (a) contacting a biological sample obtained from a patient with a
- 15 binding agent that binds to a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;
- (b) detecting in the sample an amount of polypeptide that binds to
- 20 the binding agent; and
- (c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

25 41. A method according to claim 40, wherein the binding agent is an antibody.

42. A method according to claim 43, wherein the antibody is a monoclonal antibody.

30

43. A method according to claim 40, wherein the cancer is breast

cancer.

44. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

- 5 (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;
- 10 (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
- (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polypeptide detected in step (c) to the
- 15 amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

45. A method according to claim 44, wherein the binding agent is an antibody.

20

46. A method according to claim 45, wherein the antibody is a monoclonal antibody.

47. A method according to claim 44, wherein the cancer is a breast

25 cancer.

48. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

- 30 (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence

recited in any one of SEQ ID NO: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

5 (c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

49. A method according to claim 48, wherein the amount of
10 polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

50. A method according to claim 48, wherein the amount of
polynucleotide that hybridizes to the oligonucleotide is determined using a
15 hybridization assay.

51. A method for monitoring the progression of a cancer in a patient,
comprising the steps of:

(a) contacting a biological sample obtained from a patient with an
20 oligonucleotide that hybridizes to a polynucleotide that encodes a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of a polynucleotide that
25 hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer
30 in the patient.

52. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

5 53. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

54. A diagnostic kit, comprising:

- 10 (a) one or more antibodies according to claim 11; and
(b) a detection reagent comprising a reporter group.

55. A kit according to claim 54, wherein the antibodies are immobilized on a solid support.

15

56. A kit according to claim 54, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

57. A kit according to claim 54, wherein the reporter group is
20 selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

58. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a
25 protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 or a
30 complement of any of the foregoing polynucleotides.

59. A oligonucleotide according to claim 58, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID Nos: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 5 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317.

60. A diagnostic kit, comprising:
(a) an oligonucleotide according to claim 59; and
10 (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

1/25

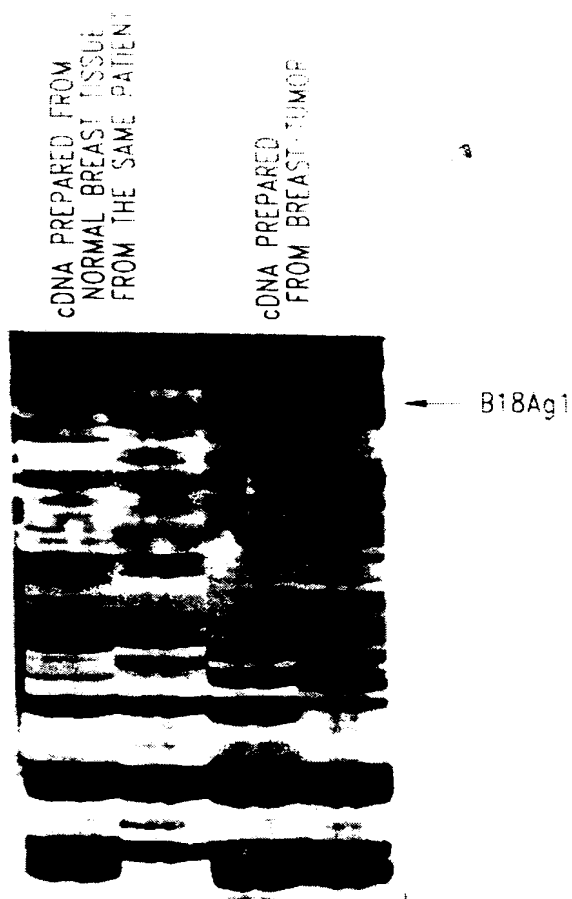


Fig. 1

SUBSTITUTE SHEET (RULE 26)

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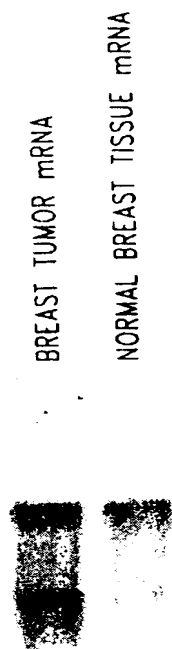


Fig. 2

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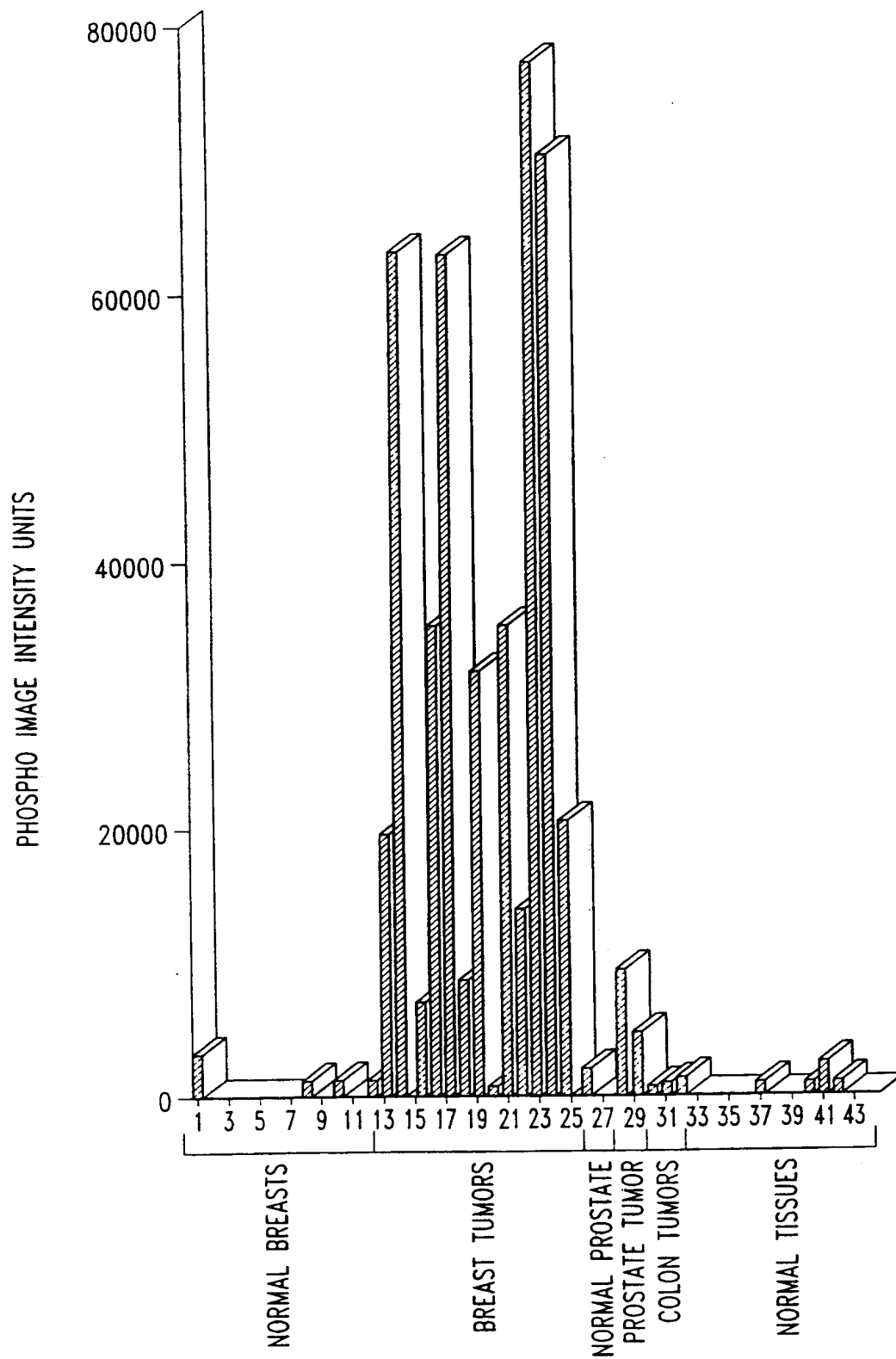


Fig. 3

SUBSTITUTE SHEET (RULE 26)

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GENOMIC CLONE MAP

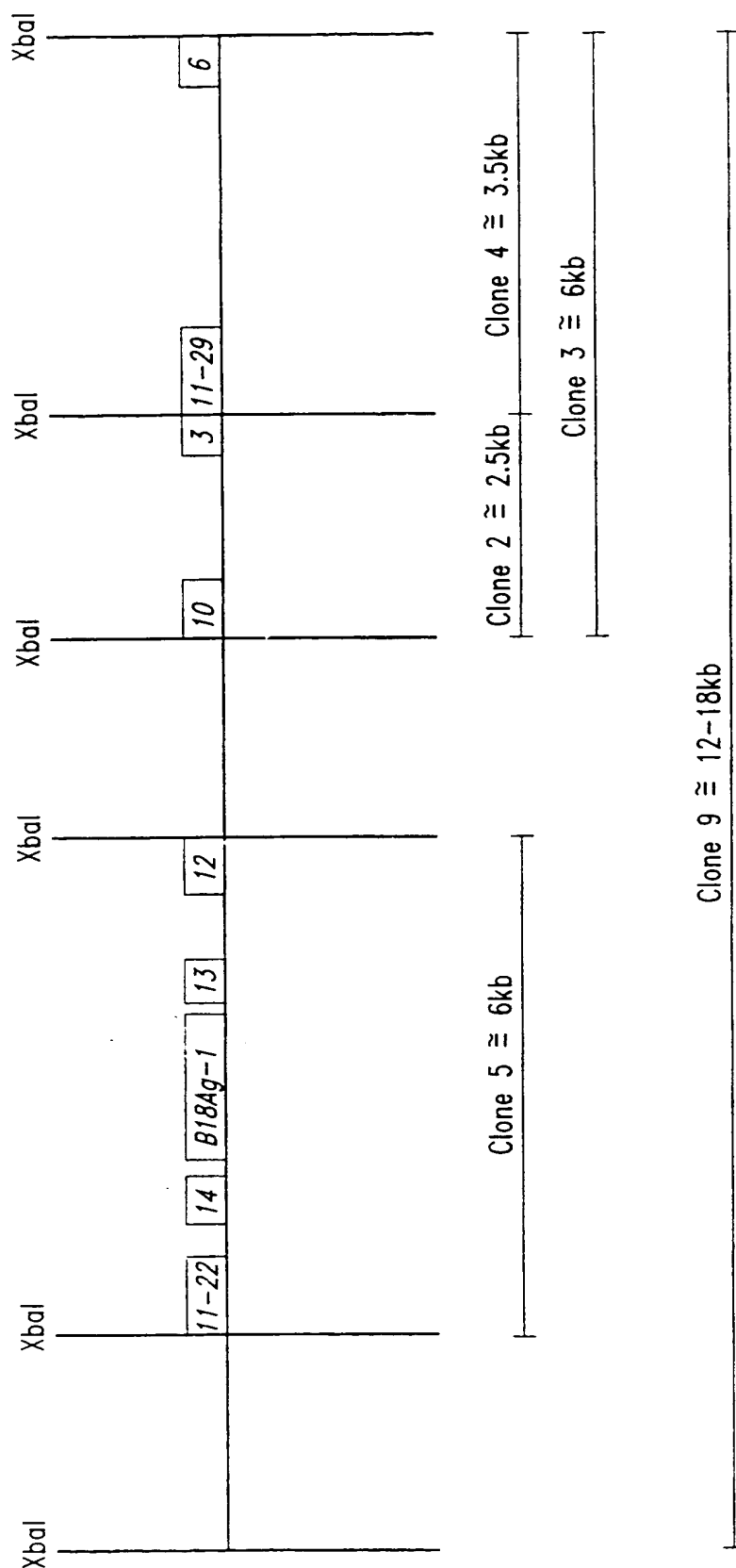


Fig. 4

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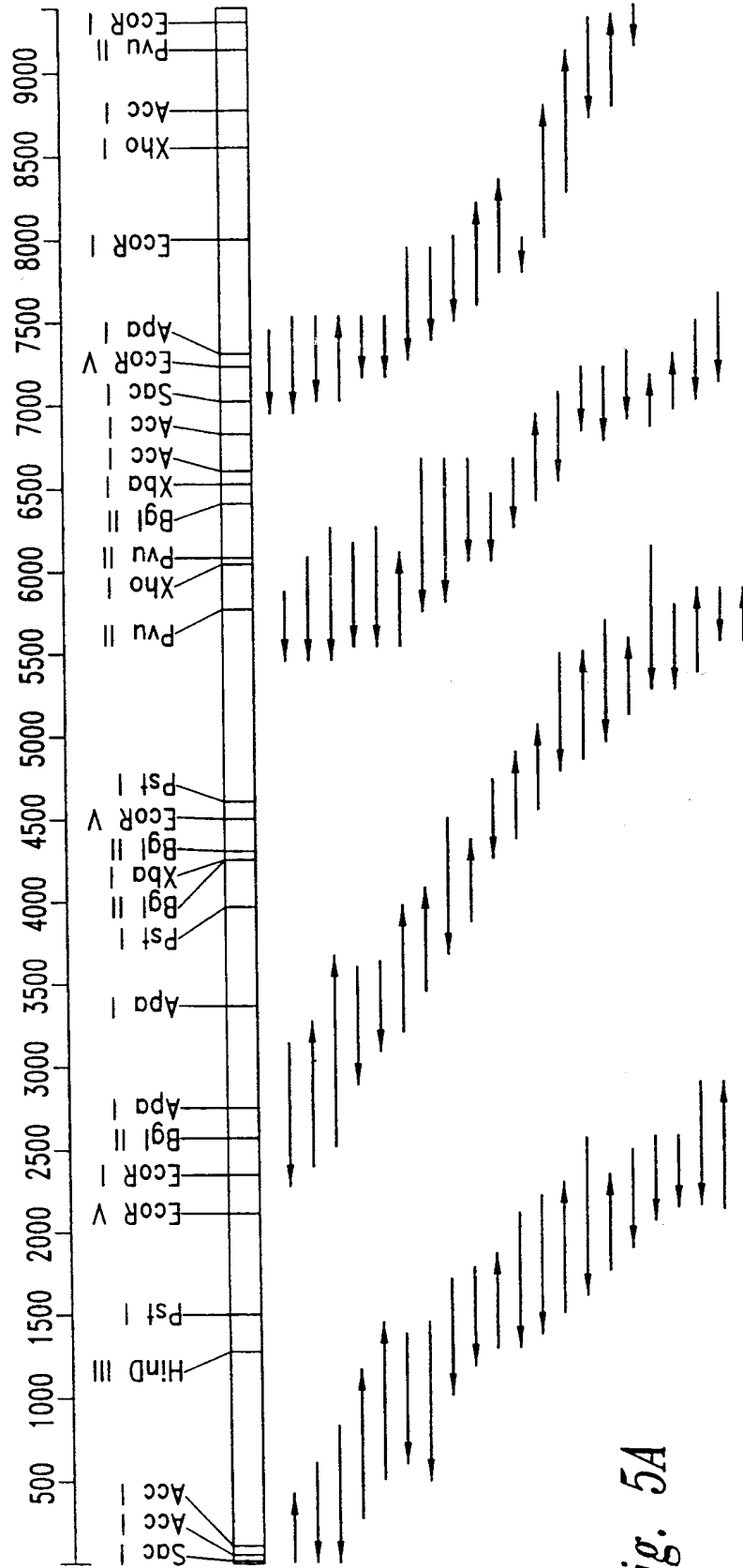


Fig. 5A

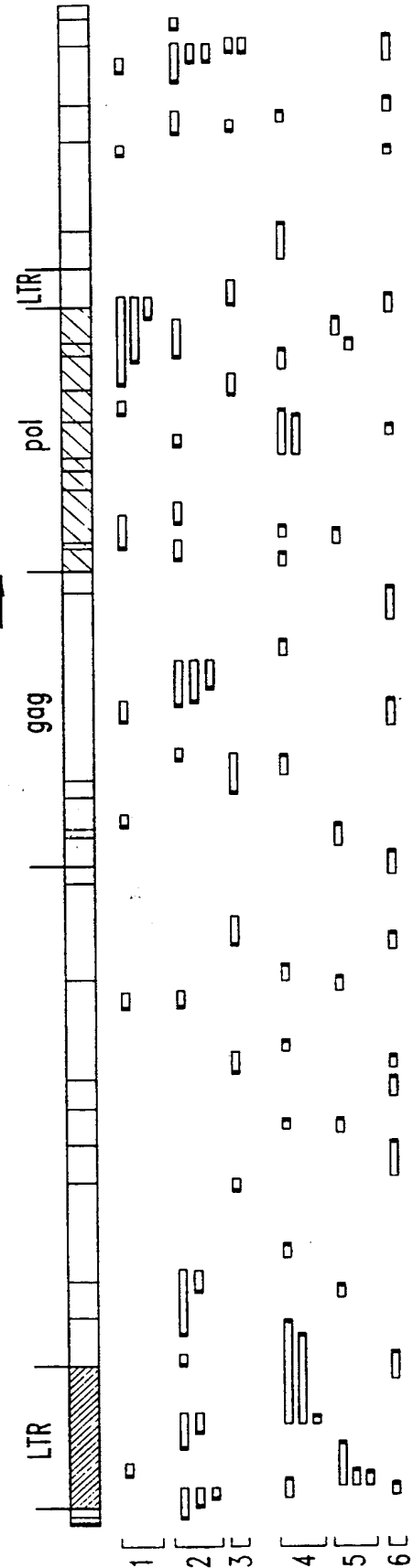


Fig. 5B

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B18Ag1

TTA	GAG	ACC	CAA	TTG	GGA	CCT	AAT	TGG	GAC	CCA	AAT	TTC	TCA	AGT	GGA	48
Leu	Glu	Thr	Gln	Leu	Gly	Pro	Asn	Trp	Asp	Pro	Asn	Phe	Ser	Ser	Gly	
1				5				10					15			
GGG	AGA	ACT	TTT	GAC	GAT	TTC	CAC	CGG	TAT	CTC	CTC	GTG	GGT	ATT	CAG	96
Gly	Arg	Thr	Phe	Asp	Asp	Phe	His	Arg	Tyr	Leu	Leu	Val	Gly	Ile	Gln	
			20					25					30			
GGA	GCT	GCC	CAG	AAA	CCT	ATA	AAC	TTG	TCT	AAG	GCG	ATT	GAA	GTC	GTC	144
Gly	Ala	Ala	Gln	Lys	Pro	Ile	Asn	Leu	Ser	Lys	Ala	Ile	Glu	Val	Val	
		35					40					45				
CAG	GGG	CAT	GAT	GAG	TCA	CCA	GGA	GTG	TTT	TTA	GAG	CAC	CTC	CAG	GAG	192
Gln	Gly	His	Asp	Glu	Ser	Pro	Gly	Val	Phe	Leu	Glu	His	Leu	Gln	Glu	
	50					55					60					
GCT	TAT	CGG	ATT	TAC	ACC	CCT	TTT	GAC	CTG	GCA	GCC	CCC	GAA	AAT	AGC	240
Ala	Tyr	Arg	Ile	Tyr	Thr	Pro	Phe	Asp	Leu	Ala	Ala	Pro	Glu	Asn	Ser	
65					70				75						80	
CAT	GCT	CTT	AAT	TTG	GCA	TTT	GTG	GCT	CAG	GCA	GCC	CCA	GAT	AGT	AAA	288
His	Ala	Leu	Asn	Leu	Ala	Phe	Val	Ala	Gln	Ala	Ala	Pro	Asp	Ser	Lys	
				85					90					95		
AGG	AAA	CTC	CAA	AAA	CTA	GAG	GGA	TTT	TGC	TGG	AAT	GAA	TAC	CAG	TCA	336
Arg	Lys	Leu	Gln	Lys	Leu	Glu	Gly	Phe	Cys	Trp	Asn	Glu	Tyr	Gln	Ser	
			100				105						110			
GCT	TTT	AGA	GAT	AGC	CTA	AAA	GGT	TTT								363
Ala	Phe	Arg	Asp	Ser	Leu	Lys	Gly	Phe								
		115					120									

Fig. 6

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B17Ag1

GC TGGGCACAGT GGCTCATACC TGTAATCCTG ACCGTTTCAG AGGCTCAGGT	60
CG CTTGAGCCCA AGATTTCAG ACTAGTCTGG GTAACATAGT GAGACCCTAT	120
AA AAATAAAAAA ATGAGCCTGG TGTAGTGGCA CACACCAGCT GAGGAGGGAG	180
CT AGGAGA	196

Fig. 7

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B17Ag2

GC TTGGGGGCTC TGACTAGAAA TTCAAGGAAC CTGGGATTCA AGTCCAACTG	60
AC TTACACTGTG GNCTCCAATA AACTGCTTCT TTCCTATTCC CTCTCTATTA	120
AA GGAAAACGAT GTCTGTGTAT AGCCAAGTCA GNTATCCTAA AAGGAGATAC	180
AT TAAATATCAG AATGTAAAAC CTGGGAACCA GGTTCCTCAGC CTGGGATTAA	240
CA AGAAGACTGA ACAGTACTAC TGTGAAAAGC CCGAAGNGGC AATATGTTCA	300
TT GAAGGATGGC TGGGAGAATG AATGCTCTGT CCCCCAGTCC CAAGCTCACT	360
CT CCTTTATAGC CTAGGAGA	388

Fig. 8

9/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag2a

GC CTATAATCAT GTTCTCATT ATTTTCACAT TTTATTAACC AATTTCTGTT	60
AA AATATGAGGG AAATATATGA AACAGGGAGG CAATGTTTCAG ATAATTGATC	120
TG ATTTCTACAT CAGATGCTCT TTCCTTTCCT GTTTATTTCC TTTTATTTT	180
GG TCGAATGTAA TAGCTTTGTT TCAAGAGAGA GTTTTGGCAG TTTCTGTAGC	240
CT GCTCATGTCT CCAGGCATCT ATTTGCACTT TAGGAGGTGT CGTGGGAGAC	300
CT ATTTTTTCCA TATTTGGGCA ACTACTA	337

Fig. 9

10/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag1b

GC CATACAGTGC CTTTCCATTT ATTTAACCCC CACCTGAACG GCATAAACTG	60
GC TGGTGTTTTT TACTGTAAAC AATAAGGAGA CTTTGCTCTT CATTTAAACC	120
AT TTCATATTTT ACGCTCGAGG GTTTTTACCG GTTCCTTTTT ACACTCCTTA	180
TT TAAGTCGTTT GGAACAAGAT ATTTTTTCTT TCCTGGCAGC TTTTAACATT	240
TT TGTGTCTGGG GGACTGCTGG TCACTGTTTC TCACAGTTGC AAATCAAGGC	300
CC AAGAAAAAAA AATTTTTTTG TTTTATTTGA AACTGGACCG GATAAACGGT	360
CG GCTGCTGTAT ATAGTTTTAA ATGGTTTATT GCACCTCCTT AAGTTGCACT	420
GG GGGGNTTTTG NATAGAAAGT NTTTANTCAC ANAGTCACAG GGACTTTTNT	480
NA CTGAGCTAAA AAGGGCTGNT TTTCGGGTGG GGGCAGATGA AGGCTCACAG	540
TC TCTTAGAGGG GGGAACNCT A	571

Fig. 10

11/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag1a

TA ATAACTTAAA TATATTTTGA TCACCCACTG GGGTGATAAG ACAATAGATA	60
TT TCCAAAAAGC ATAAAACCAA AGTATCATAC CAAACCAAAT TCATACTGCT	120
CC GCACTGAAAC TTCACCTTCT AACTGTCTAC CTAACCAAAT TCTACCCTTC	180
GG TGC GTGCTCA CTACTCTTTT TTTTTTTTTT TTTNTTTTGG AGATGGAGTC	240
CA GCCCAGGGGT GGAGTACAAT GGCACAACCT CAGCTCACTG NAACCTCCGC	300
TT CATGAGATTC TCCTGNTTCA GCCTTCCCAG TAGCTGGGAC TACAGGTGTG	360
TG CCTGGNTAAT CTTTTTTNGT TTTNGGGTAG AGATGGGGGT TTTACATGTT	420
TG GTNTCGAACT CCTGACCTCA AGTGATCCAC CCACCTCAGG CTCCCAAAGT	480
TA CAGACATGAG CCACTGNGCC CAGNCCTGGT GCATGCTCAC TTCTCTAGGC	540
	548

Fig. 11

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B11Ag1

TG CACATGCAGA ATATTCTATC GGTACTTCAG CTATTACTCA TTTTGATGGC	60
AG CCTATCCTCA AGATGAGTAT TTAGAAAGAA TTGATTTAGC GATAGACCAA	120
GC ACTCTGACTA CACGAAATTG TTCAGATGTG ATGGATTTAT GACAGTTGAT	180
GA GATTATTAAG TGATTATTTT AAAGGGAATC CATTAAATCC AGAATATCTT	240
TC AAGATGATAT AGAAATAGAA CAGAAAGAGA CTACAAATGA AGATGTATCA	300
TA TTGAAGAGCC TATAGTAGAA AATGAATTAG CTGCATTTAT TAGCCTTACA	360
TT TTCCTGATGA ATCTTATATT CAGCCATCGA CATAGCATTG CCTGATGGGC	420
GA ATAATAGAAA CTGGGTGCGG GGCTATTGAT GAATTCATCC NCAGTAAATT	480
AC AAAATATAAC TCGATTGCAT TTGGATGATG GAATACTAAA TCTGGCAAAA	540
GG AGCTACTAGT AACCTCTCTT TTTGAGATGC AAAATTTTCT TTTAGGGTTT	600
CT ACTTTACGGA TATTGGAGCA TAACGGGA	638

Fig. 12

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA3c

```
ACTGATGGAT GTCGCCGGAG GCGAGGGGCC TTATCTGATG CTCGGCTGCC TGTCGTGAT   60
GTGCGCGGGCG ATTGGGCTGT TTATCTCAA CACCGCCACG GCGGTGCTGA TGGCGCCTAT  120
TGCCTTAGCG GCGGCGAAGT CAATGGGCGT CTCACCCTAT CCTTTTGCCA TGGTGGTGGC  180
GATGGCGGGCT TCGGCGGGCT TTATGACCCC GGTCTCCTCG CCGGTTAACA CCCTGGTGCT  240
TGGCCCTGGC AAGTACTCAT TTAGCGATTT TGTCAAATA GCGGTG                               286
```

Fig. 13

14/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B9CG1

AG CAGCCCCTTC TTCTCAATTT CATCTGTCAC TACCCTGGTG TAGTATCTCA	60
CA TTTTATAGC CTCCTCCCTG GTCTGTCTTT TGATTTTCCT GCCTGTAATC	120
AC ATAAGTGCAA GTAAACATTT CTAAAGTGTG GTTATGCTCA TGTCACCTCT	180
AA ATAGTTTCCA TTACCGTCTT AATAAAATTC GGATTTGTTC TTTNCTATTN	240
CA CCTATGACCG AA	262

Fig. 14

15/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B9CG3

AG CAAAGCCAGT GGTTTGAGCT CTCTACTGTG TAAACTCCTA AACCAAGGCC	60
TA AATGGTGGCA GGATTTTAT TATAACATG TACCCATGCA AATTCCTAT	120
GA TATATTCTTC TACATTTAAA CAATAAAAAT AATCTATTTT TAAAAGCCTA	180
AG TTAGGTAAGA GTGTTTAATG AGAGGGTATA AGGTATAAAT CACCAGTCAA	240
TG CCTATGACCG A	261

Fig. 15

16/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B2CA2

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCGT	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 16

17/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA1

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCTG	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 17

18/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA2

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCTG	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCAANG ATCTTCAT	208

Fig. 18

19/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA3

AG GGAGCAAGGA GAAGGCATGG AGAGGCTCAN GCTGGTCCTG GCCTACGACT	60
CT GTCGCCGGGG ATGGTGGAGA ACTGAAGCGG GACCTCCTCG AGGTCCTCCG	120
TC NCCGTCCAGG AGGAGGGTCT TTCCGTGGTC TNGGAGGAGC GGGGGGAGAA	180
TC ATGGTCNACA TCCC	204

Fig. 19

20/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B4CA1

TC AGGAGCGGGT AGAGTGGCAC CATTGAGGGG ATATTCAAAA ATATTATTTT	60
TG ATAGTTGCTG AGTTTTTCTT TGACCCATGA GTTATATTGG AGTTTATTTT	120
CC AATCGCATGG ACATGTTAGA CTTATTTTCT GTTAATGATT NCTATTTTAA	180
GA TTTGAGAAAT TGGTTNTTAT TATATCAATT TTTGGTATTT GTTGAGTTTG	240
GC TTAGTATGTG ACCA	264

Fig. 20

21/25

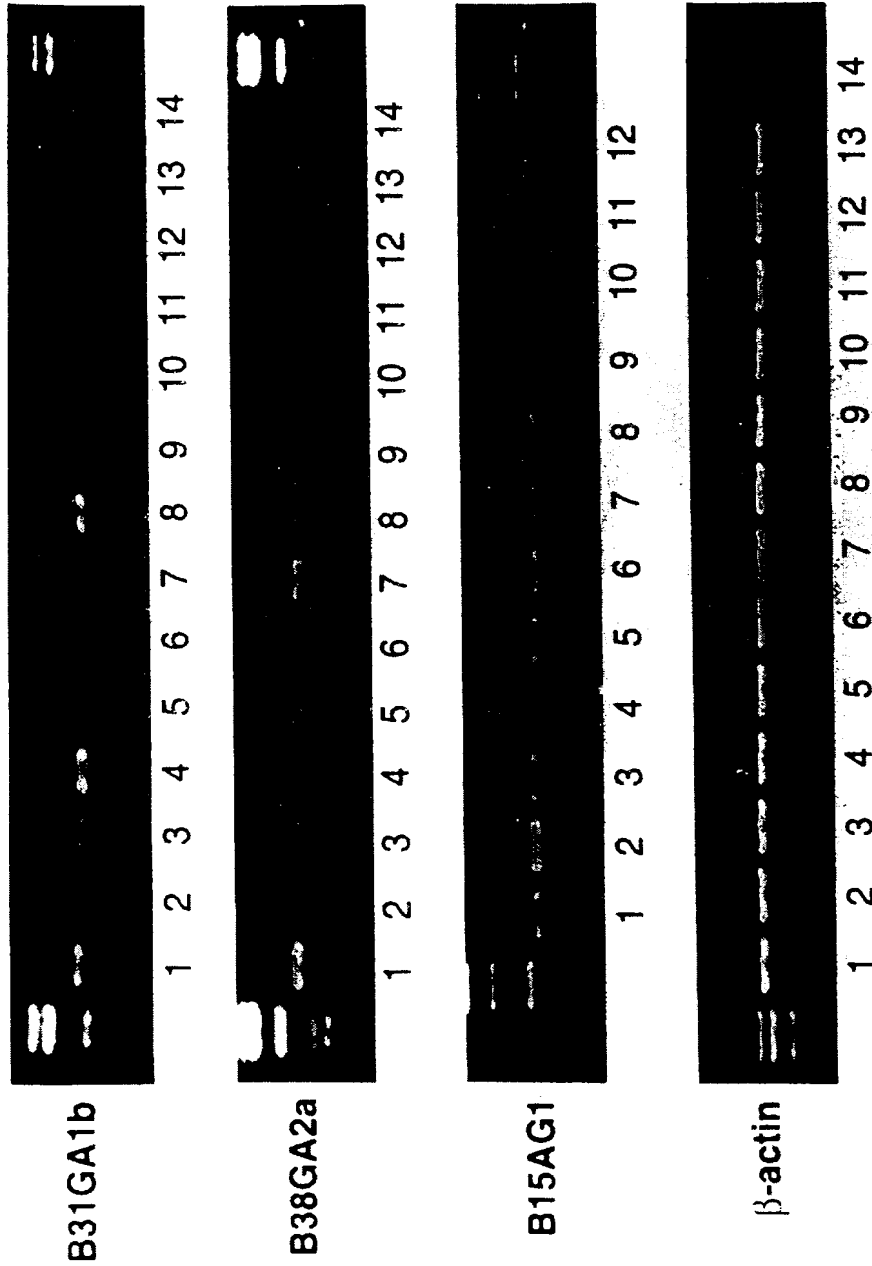


Fig. 21A

SUBSTITUTE SHEET (RULE 26)

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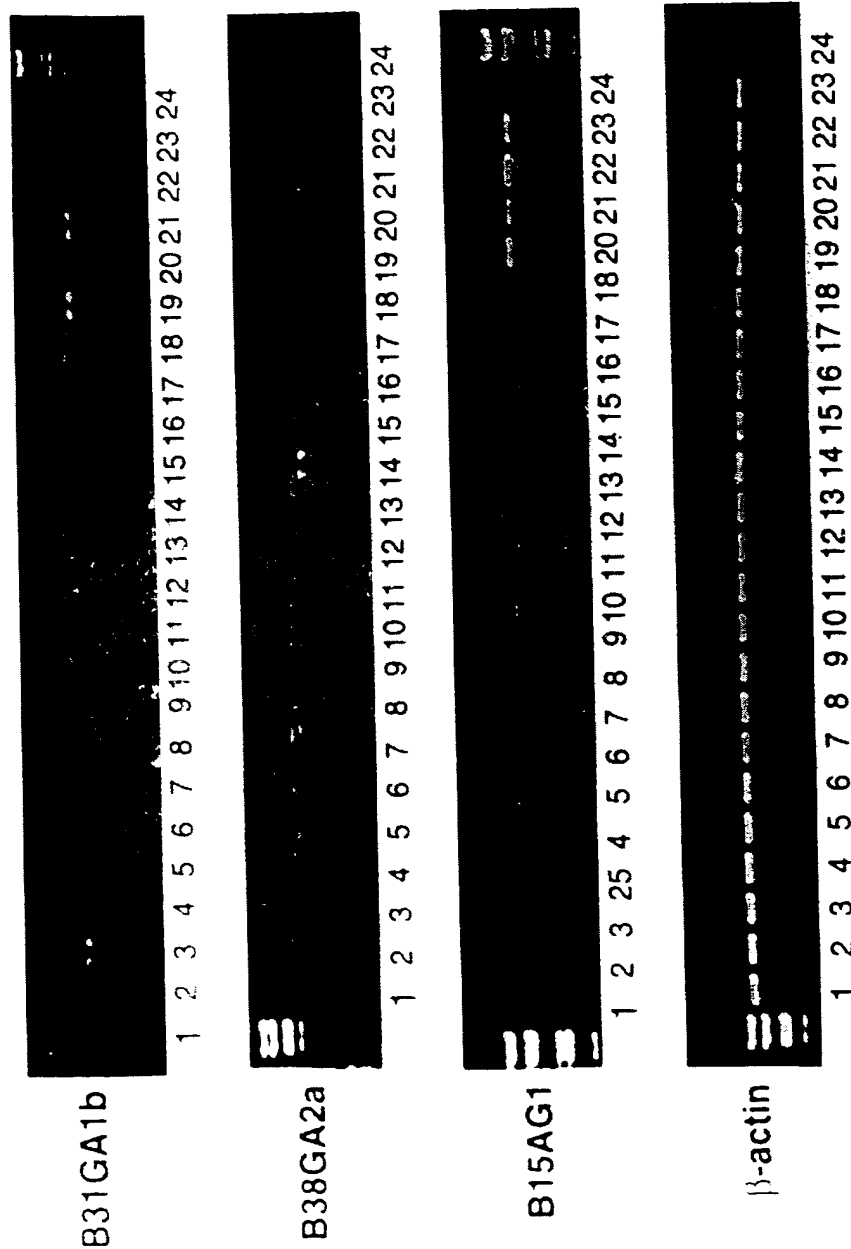


Fig. 21B

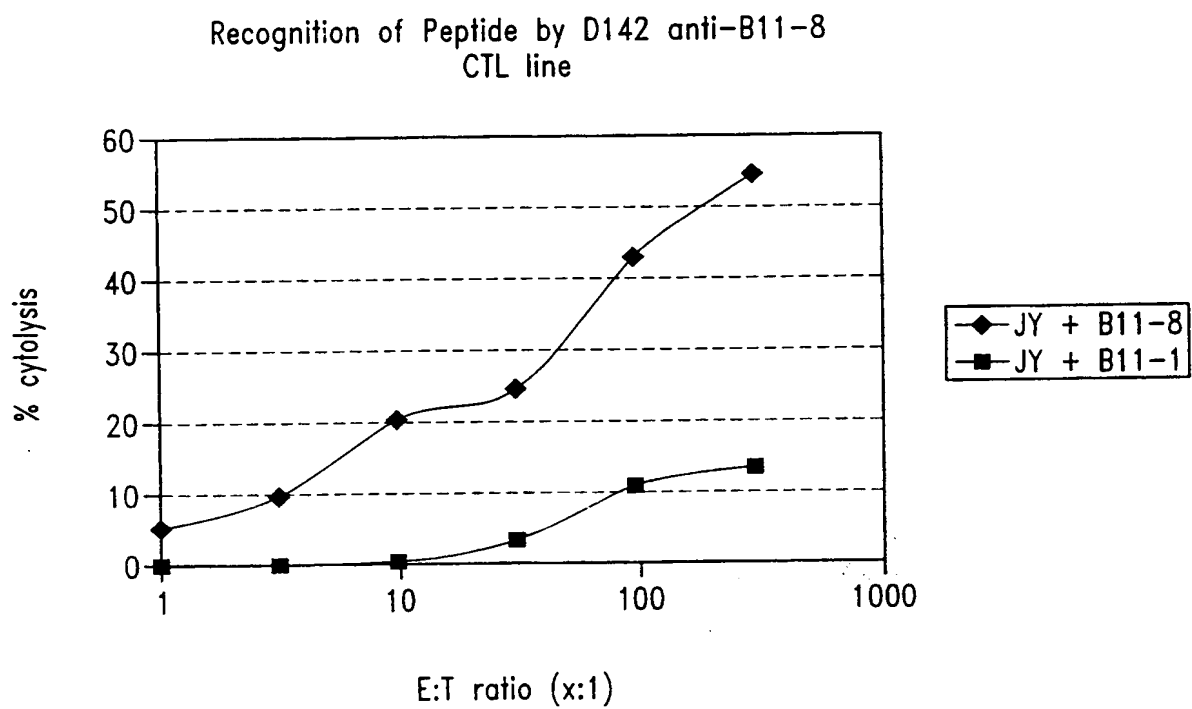


Fig. 22

24/25

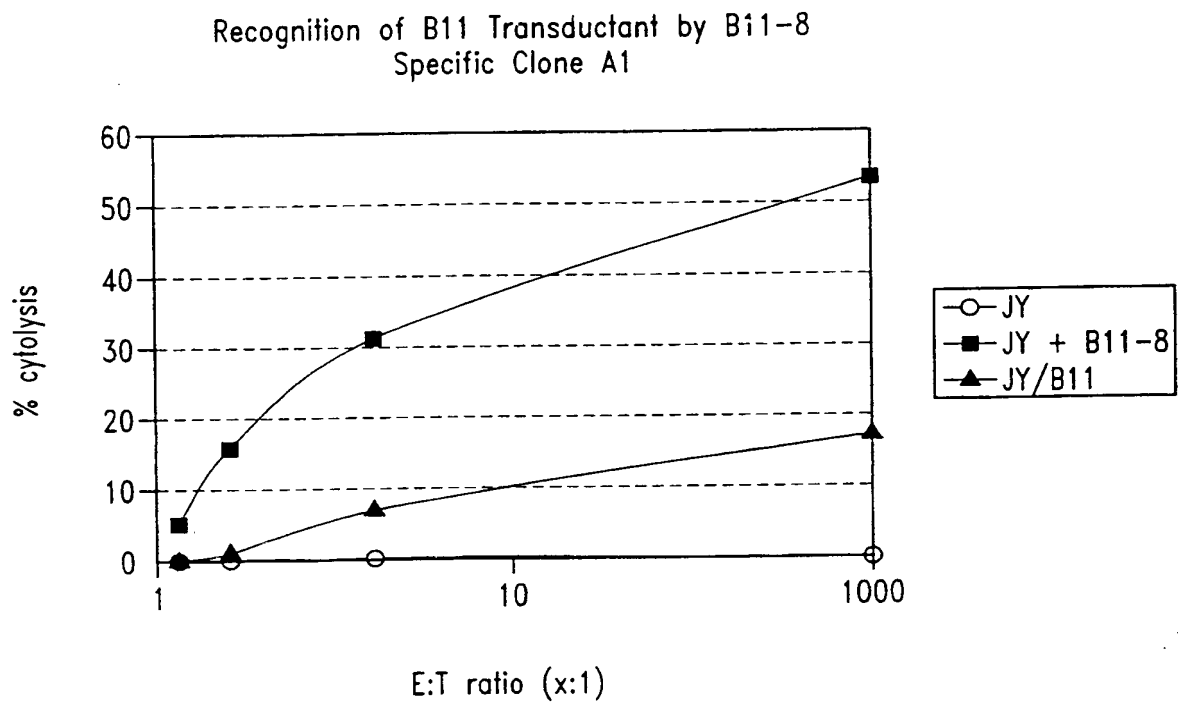


Fig. 23

25/25

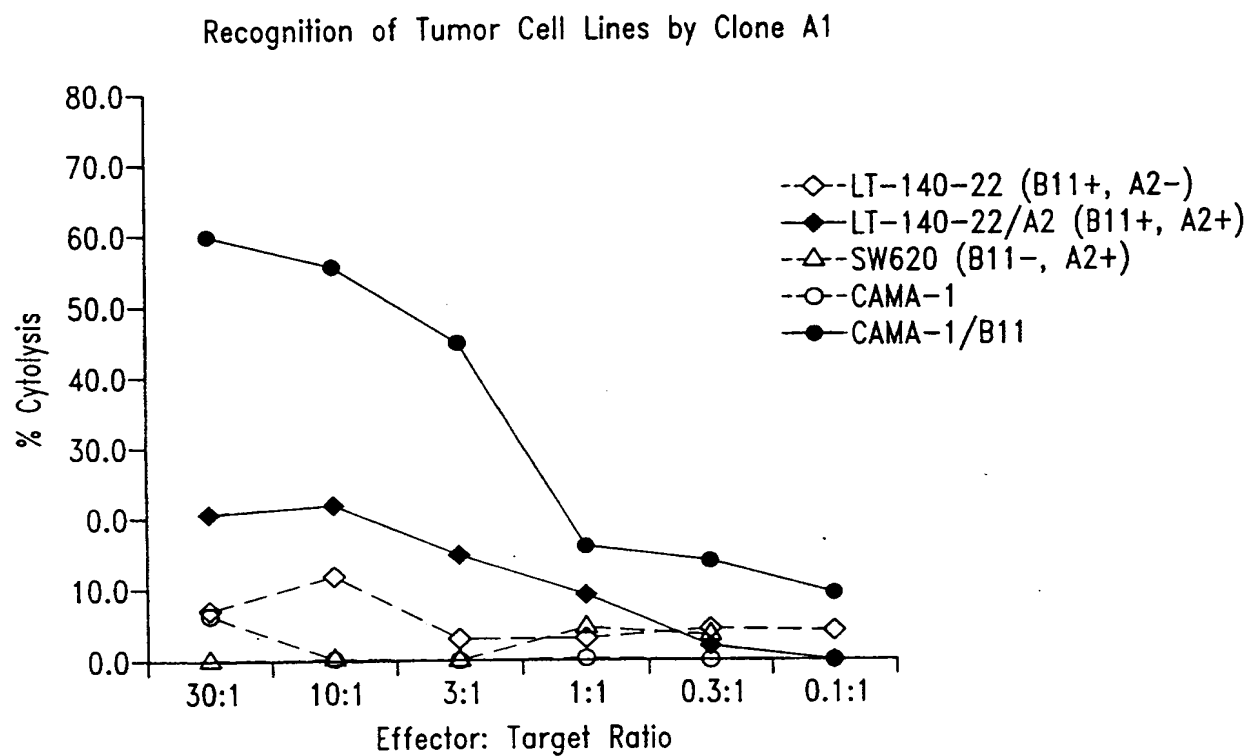


Fig. 24
SUBSTITUTE SHEET (RULE 26)

SEQUENCE LISTING

<110> Corixa Corporation

<120> COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER

<130> 210121.41926PC

<140> PCT

<141> 2000-04-07

<160> 317

<170> FastSEQ for Windows Version 3.0

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cacctccagg aggcttatcg gatttacacc ccttttgacc tggcagcccc cgaaaatagc	240
catgctctta atttggcatt tgtggctcag gcagccccag atagtataag gaaactccaa	300
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ttt	363

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<211> 121

<212> PRT

<213> Homo sapien

<400> 2

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Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Ala Ile Glu Val Val	
35 40 45	
Gln Gly His Asp Glu Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu	
50 55 60	
Ala Tyr Arg Ile Tyr Thr Pro Phe Asp Leu Ala Ala Pro Glu Asn Ser	
65 70 75 80	
His Ala Leu Asn Leu Ala Phe Val Ala Gln Ala Ala Pro Asp Ser Lys	
85 90 95	
Arg Lys Leu Gln Lys Leu Glu Gly Phe Cys Trp Asn Glu Tyr Gln Ser	
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<212> DNA

<213> Homo sapien

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<223> n = A,T,C or G

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tcttcaaagc	ctaacagatc	aagcagctct	ccggtgcaca	acctgcgccc	aggtaaattgc	180
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aaacncccc	ctccaanccc	cggccnaagn	ggaagggtcc	cttgaatccc	ncctccncca	960
anggcccgga	accnttaaan	tngttccngg	gggttnggcc	taaaagnccn	atttggtaaa	1020
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<210> 4

<211> 1087

<212> DNA

<213> Homo sapien

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aaaacggant	cttgctccgt	tgtccangct	gggaattttt	ttttggccaa	tctccgctnc	660
cttgcaanaa	tnctgcntcc	caaaattacc	ncctttttcc	cacctccacc	ccnnggaatt	720
acctggaatt	anaggccccc	cccccccccc	cggctaattt	gtttttgttt	ttagtaaaaa	780
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aggcaggngg	ttcttcccga	acttccaatt	ncaacagecn	tgcccattgn	tgaaaccctt	840
ttcctaaaat	taaaaaatan	ccggttnngg	nnggcctctt	ccccctceng	gnggggnngg	900
aaantcctta	ccccnaaaaa	ggttgcttag	ccccngtcc	ccactcccc	nggaaaaatn	960
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<210> 6
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 <213> Homo sapien
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cnnnccnct	neccnccnnt	tenentcnnn	ntecnnccnn	ntcnncnnnn	cnnnncntnn	420
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agaaaaattc	ttctgccttg	agatgctgtt	aatctgtaac	ccctagcccca	accctgtgct	180
cacagagaca	tgtgctgtgt	tgactcaagg	ttcaatggat	ttagggtat	gctttgttaa	240
aaaagtgtt	gaagataata	tgcttgtaa	aagtcacac	cattctctaa	tctcaagtac	300
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<212> DNA

<213> Homo sapien

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<213> Homo sapien

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caatgcattc	tgagctgctg	aatcagcttt	ctggttacca	cgggcaacag	ccgtgttttc	300
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taatatcctt	accccatcgg	agagcctgag	tgaggggcgt	caattcagcc	cttttggtgt	480
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accgg						545

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 <212> DNA
 <213> Homo sapien

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agattttcaag	
actagtctgg	
gtaacatagt	
gagaccctat	
ctctacgaaa	180
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aatcgagcct	196
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ttcctattcc	
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aaataaataa	180
ggaaaacgat	
gtctgtgtat	
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gntatcctaa	
aaggagatac	
taagtgcacat	240
taaatatcag	
aatgtaaaac	
ctgggaacca	
ggttcccagc	
ctgggattaa	
actgacagca	300
agaagactga	
acagtactac	
tgtgaaaagc	
ccgaagnggc	
aatatgttca	
ctctaccgtt	360
gaaggatggc	
tgggagaatg	
aatgctctgt	
cccccagtc	
caagctcact	
tactataacct	388
cctttatagc	
ctaggaga	

<210> 13
 <211> 337
 <212> DNA
 <213> Homo sapien

<400> 13	
tagtagttgc	60
ctataatcat	
gtttctcatt	
attttcacat	
tttattaacc	
aatttctggt	
taccctgaaa	120
aatatgaggg	
aaatatatga	
aacagggagg	
caatgttcag	
ataattgatc	
acaagatatg	180
atttctacat	
cagatgctct	
ttcctttcct	
gtttatttcc	
tttttatttc	
ggttgtgggg	240
tcgaatgtaa	
tagctttgtt	
tcaagagaga	
gttttggcag	
tttctgtagc	
ttctgacact	300
gctcatgtct	
ccaggcatct	
atttgcactt	
taggaggtgt	
cgtgggagac	
tgagaggtct	337
attttttcca	
tatttgggca	
actacta	

<210> 14
 <211> 571
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (571)

<223> n = A,T,C or G

<400> 14

tagtagttgc	catacagtgc	ctttccattt	atttaacccc	cacctgaacg	gcataaactg	60
agtgttcagc	tgggtgtttt	tactgtaaac	aataaggaga	ctttgctctt	catttaaacc	120
aaaatcatat	ttcatatttt	acgctcgagg	gtttttaccg	gttccttttt	acactcctta	180
aaacagtttt	taagtcgttt	ggaacaagat	atTTTTtctt	tcctggcagc	ttttaacatt	240
atagcaaatt	tgtgtctggg	ggactgctgg	tcactgtttc	tcacagttgc	aaatcaaggc	300
atTTgcaacc	aagaaaaaaa	aatttttttg	ttttatttga	aactggaccg	gataaacggt	360
gtttggagcg	gctgctgtat	atagttttta	atgggtttatt	gcacctcctt	aagttgcact	420
tatgtggggg	ggggnTTTTg	natagaaagt	ntttantcac	anagtcacag	ggacttttnt	480
cttttggnna	ctgagctaaa	aagggctgnt	tttcgggtgg	gggcagatga	aggctcacag	540
gaggcctttc	tcttagaggg	gggaactnct	a			571

<210> 15

<211> 548

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (548)

<223> n = A,T,C or G

<400> 15

tatatattta	ataacttaaa	tatatTTtga	tcaccactg	gggtgataag	acaatagata	60
taaaagtatt	tcacaaaagc	ataaaaacaa	agtatcatac	caaaccacaa	tcatactgct	120
tccccacccc	gcaactgaaac	ttcaccttct	aactgtctac	ctaaccacaa	tctacccttc	180
aagtcttttg	tgcgtgctca	ctactctttt	TTTTTTTTt	tttnttttgg	agatggagtc	240
tggctgtgca	gcccaggggg	ggagtacaat	ggcacacact	cagctcactg	naacctccgc	300
ctcccagggt	catgagattc	tcctgnttca	gccttcccag	tagctgggac	tacagggtgtg	360
catcaccatg	cctggntaat	cttttttngt	tttngggtag	agatgggggt	tttacctgtt	420
ggccaggntg	gtntcgaaact	cctgacctca	agtgateccac	ccacctcagg	ctcccaaagt	480
gctaggatta	cagacatgag	ccactgngcc	cagnctgggt	gcatgctcac	ttctctaggg	540
aactacta						548

<210> 16

<211> 638

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (638)

<223> n = A,T,C or G

<400> 16

ttccgttatg	cacatgcaga	atattctatc	ggctacttcag	ctattactca	ttttgatggc	60
gcaatccgag	cctatcctca	agatgagtat	ttagaaagaa	ttgatttagc	gatagaccaa	120
gctggtaagc	actctgacta	cacgaaattg	ttcagatgtg	atggatttat	gacagttgat	180

ctttggaaga gattattaag tgattattht aaaggggaatc cattaattcc agaatatctt	240
ggttttagctc aagatgatat agaaatagaa cagaaagaga ctacaaatga agatgtatca	300
ccaactgata ttgaagagcc tatagtagaa aatgaattag ctgcatttat tagccttaca	360
catagcgatt ttcttgatga atcttatatt cagccatcga catagcatta cctgatgggc	420
aaccttacga ataatagaaa ctgggtgcgg ggctattgat gaattcatcc ncagtaaatt	480
tggaatnac aaaatataac tcgattgcat ttggatgatg gaatactaaa tctggcaaaa	540
gtaactttgg agctactagt aacctctctt tttgagatgc aaaattttct tttagggttt	600
cttattctct actttacgga tattggagca taacggga	638

<210> 17
 <211> 286
 <212> DNA
 <213> Homo sapien

<400> 17	
actgatggat gtgcgcggag ggcagggggcc ttatctgatg ctcggtgcc tgttcgtgat	60
gtgcgcggcg attgggctgt ttatctcaaa caccgccacg gcgggtgctga tggcgccctat	120
tgccttagcg gcggcggaagt caatgggcgt ctccacctat ccttttgcca tgggtggggc	180
gatggcggct tcggcggcgt ttatgacccc ggtctcctcg ccggttaaca ccctgggtgct	240
tggccctggc aagtactcat ttagcgattt tgcataaata ggcgtg	286

<210> 18
 <211> 262
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(262)
 <223> n = A,T,C or G

<400> 18	
tcgggtcatag cagccccttc ttctcaattt catctgtcac taccctgggtg tagtatctca	60
tagccttata tttttatagc ctctccctg gtctgtcttt tgattttcct gcctgtaatc	120
catatcacac ataactgcaa gtaaacattt cttaaagtgtg gttatgtca tgcactcct	180
gtgncaagaa atagtttcca ttaccgtctt aataaaattc ggatttggtc ttttctattn	240
tcactcttca cctatgaccg aa	262

<210> 19
 <211> 261
 <212> DNA
 <213> Homo sapien

<400> 19	
tcgggtcatag caaagccagt ggtttgagct ctctactgtg taaactccta aaccaaggcc	60
atztatgata aatgggtggca ggatttttat tataaacatg taccatgca aatttcctat	120
aactctgaga tatattcttc tacatttaaa caataaaaaat aatctatttt taaaagccta	180
atttgcgtag ttaggtaaga gtgtttaatg agagggtata aggtataaat caccagtcga	240
cgtttctctg cctatgaccg a	261

<210> 20
 <211> 294
 <212> DNA
 <213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(294)
<223> n = A,T,C or G

<400> 20
tacaacgagg cgacgtcggg aaaatcggac atgaagccac cgctgggtctt ttcgtccgag 60
cgataggcgc cggccagcca gcggaacggg tgcccggatg gcgaagcgag ccggagttct 120
tcggactgag tatgaatctt gttgtgaaaa tactcgccgc cttcgttcga cgacgtcgcg 180
tcgaaatctt cganctcctt acgatcgaag tcttcgtggg cgacgatcgc ggtcagttcc 240
gccccaccga aatcatgggt gagccggatg ctgnccccga agnccctcgt tgtn 294

<210> 21
<211> 208
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(208)
<223> n = A,T,C or G

<400> 21
ttggtaaagg gcatggacgc agacgcctga cgtttggtctg aaaatctttc attgattcgt 60
atcaatgaat aggaaaattc ccaaagaggg aatgtcctgt tgctcgccag tttttntggt 120
gttctcatgg anaaggcaan gagctcttca gactattggn attntcgttc ggtctctcgc 180
caactagtcg ncttgcnang atcttcat 208

<210> 22
<211> 287
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(287)
<223> n = A,T,C or G

<400> 22
nccnttgagc tgagtgattg agatntgtaa tggttgtaag ggtgattcag gcggattagg 60
gtggcggggt acccggcagt ggggtctccc acaggccagc aggatttggg gcaggtagcg 120
ngtgcgcatc gctcgactat atgctatggc aggcgagccg tggaaggngg atcaggtcac 180
ggcgctggag ctttccacgg tccatgnatt gngatggctg ttctaggcgg ctggtgccaa 240
gcgtgatggt acgctggctg gagcattgat ttctggtgcc aaggtgg 287

<210> 23
<211> 204
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(204)
<223> n = A,T,C or G

<400> 23
 ttgggtaaaag ggagcaagga gaaggcatgg agaggctcan gctggctctg gcctacgact 60
 gggccaagct gtcgccgggg atggtggaga actgaagcgg gacctcctcg aggtcctccg 120
 ncgttacttc nccgtccagg aggaggggtct ttccgtggtc tnggaggagc ggggggagaa 180
 gatnctcctc atggtcnaca tccc 204

<210> 24
 <211> 264
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(264)
 <223> n = A,T,C or G

<400> 24
 tggattggtc aggagcgggt agagtggcac cattgagggg atattcaaaa atattatttt 60
 gtcctaaaatg atagttgctg agtttttctt tgacctatga gttatattgg agtttatttt 120
 ttaactttcc aatcgcatgg acatgttaga cttattttct gttaatgatt nctattttta 180
 ttaaattgga tttagaaaat tggttnttat tatatcaatt tttgggtattt gttgagtttg 240
 acattatagc ttagtatgtg acca 264

<210> 25
 <211> 376
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(376)
 <223> n = A,T,C or G

<400> 25
 ttacaacgag gggaaactcc gtctctacaa aaattaaaaa attagccagg tgtgggtgggtg 60
 tgcacccgca atcccagcta cttggggaggt tgagacacaa gantcaccta natgtggggag 120
 gtcaagggtg catgagtcac gattgtgcca ctgcaactcca gcctgggtga cagaccgaga 180
 ccctgcctca anaganaang aataggaagt tcagaaatcn tggntgtggn gccagcaat 240
 ctgcatctat ncaaccctg caggcaangc tgatgcagcc tangttcaag agctgctgtt 300
 tctggaggca gcagttnggg cttccatcca gtatcacggc cacactcgca cnagccatct 360
 gtccctcgtg tgtnac 376

<210> 26
 <211> 372
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(372)
 <223> n = A,T,C or G

<400> 26
 ttacaacgag gggaaactcc gtctctacaa aaattaaaaa attagccagg tgtgggtgggtg 60
 tgcacctgta atcccagcta cttggggcggc tgagacacaa gaaccaccta aatgtggggag 120

ggccaagggtt	gcatgagtca	tgatcgcgcc	actgcactcc	agcctgggtg	acagactgag	180
accctgcctc	aaaagaaaaa	gaataggaag	ttcagaaacc	ctgggtgtgg	ngcccagcaa	240
tctgcattta	aacaatccct	gcaggcaatg	ctgatgcagc	ctaagttcaa	gagctgctgt	300
tctggaggca	gnagtaagg	cttccatcca	gcatacggg	caacactgca	aaagcacctg	360
tcctcgttgg	ta					372

<210> 27
 <211> 477
 <212> DNA
 <213> Homo sapien

<400> 27						
ttctgtccac	atctacaagt	tttattttatt	ttgtgggttt	tcagggtgac	taagtttttc	60
cctacattga	aaagagaagt	tgctaaaagg	tgacacaggaa	atcatttttt	taagtgaata	120
tgataatatg	gggtccgtgt	taatacaact	gagacatatt	tggttctctgt	tttttttagag	180
tcacctctta	aagtccaatc	ccacaatggt	gaaaaaaaaa	tagaaagtat	ttgttctacc	240
tttaaggaga	ctgcagggat	tctccttgaa	aacggagtat	ggaatcaatc	ttaaataaat	300
atgaaattgg	ttggtcttct	gggataagaa	attcccaact	cagtgtgctg	aaattcacct	360
gacttttttt	gggaaaaaat	agtcgaaaaat	gtcaatttgg	tccataaaat	acatgttact	420
attaaaagat	atttaaagac	aaattctttc	agagctctaa	gattgggtgtg	gacagaa	477

<210> 28
 <211> 438
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(438)
 <223> n = A,T,C or G

<400> 28						
tctncaacct	cttgantgtc	aaaaaccttn	taggctatct	ctaaaagctg	actgggtattc	60
attccagcaa	aatccctcta	gtttttggag	tttcccttta	ctatctgggg	ctgcctgagc	120
cacaaatgcc	aaattaagag	catggctatt	ttcgggggct	gacagggtcaa	aaggggtgta	180
aatccgataa	gcctcctgga	ggtgctctaa	aaacactcct	ggtgactcat	catgcccctg	240
gacgacttca	atcgncttag	acaagtttat	aggtttctgg	gcagctccct	gaatacccac	300
gaggagatac	cgggtggaaat	cgtcaaaagt	tctccctcca	cttgagaaat	ttgggtccca	360
attagggtccc	aattgggtct	ctaataccta	ttcctctagc	ttcctcctcc	ggnctattgg	420
ttgatgtgag	gttgaaga					438

<210> 29
 <211> 620
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(620)
 <223> n = A,T,C or G

<400> 29						
aagaggggtac	cagccccaa	ccttgacaac	ttccataggg	tgtcaagcct	gtgggtgcac	60
agaagtcaaa	aattgagttt	tgggatcctc	agcctagatt	tcagaggata	taaagaaaca	120
cctaacacct	agatattcag	acaaaagttt	actacaggga	tgaagctttc	acggaaaacc	180

tctactagga	aagtacagaa	gagaaatgtg	ggtttgaggc	ccccaacag	aatccccctct	240
agaacactgc	ctaatagaaac	tgtgagaaga	tggccactgt	catccagaca	ccagaatgat	300
agaccaccca	aaaacttatg	ccatattgcc	tataaaacct	acagacactc	aatgccagcc	360
ccatgaaaaa	aaaactgaga	agaagactgt	nccctacaat	gccaccggag	cagaactgcc	420
ccaggccatg	gaagcacagc	tcttatatca	atgtgacctg	gatgttgaga	catggaatcc	480
nangaaatcn	ttttaanact	tccacggtn	aatgactgcc	ctattanatt	cngaacttan	540
atccnggcct	gtgacctctt	tgctttggcc	attccccctt	tttggaatgg	ctnttttttt	600
cccatgectg	tnccctctta					620

<210> 30

<211> 100

<212> DNA

<213> Homo sapien

<400> 30

ttacaacgag	gggggtcaatg	tcataaatgt	cacaataaaa	caatctcttc	tttttttttt	60
tttttttttt	tttttttttt	tttttttttt	tttttttttt			100

<210> 31

<211> 762

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(762)

<223> n = A,T,C or G

<400> 31

tagtctatgc	gccggacaga	gcagaattaa	attggaagtt	gccctccgga	ctttctaccc	60
acactcttcc	tgaaaagaga	aagaaaagag	gcaggaaaga	ggtaggatt	tcattttcaa	120
gagtcagcta	attaggagag	cagagtttag	acagcagtag	gcaccccatg	atacaaacca	180
tggacaaaagt	ccctgttttag	taactgccag	acatgatcct	gctcaggttt	tgaaatctct	240
ctgcccataa	aagatggaga	gcaggagtgc	catccacatc	aacacgtgtc	caagaaagag	300
tctcagggag	acaaggggtat	caaaaaacaa	gattcttaat	gggaaggaaa	tcaaaccaaa	360
aaattagatt	tttctctaca	tatatataat	atacagatat	ttaacacatt	attccagagg	420
tggctccagt	ccttggggct	tgagagatgg	tgaaaacttt	tgttccacat	taacttctgc	480
tctcaaattc	tgaagtatat	cagaatggga	caggcaatgt	tttgtccac	actggggcac	540
agacccaaat	ggttctgtgc	ccgaagaaga	gaagcccga	agacatgaag	gatgcttaag	600
ggggggttggg	aaagccaaat	tggtantatc	ttttcctcct	gcctgtgttc	cngaagtctc	660
cnctgaagga	attcttaaaa	ccctttgtga	ggaaatgccc	ccttaccatg	acaantgggc	720
ccattgcttt	tagggngatg	gaaacaccaa	gggttttgat	cc		762

<210> 32

<211> 276

<212> DNA

<213> Homo sapien

<400> 32

tagtctatgc	gtgtattaac	ctccccctcc	tcagtaacaa	ccaaagaggc	aggagctggt	60
attaccaacc	ccattttaca	gatgcacaa	taatgacaga	gaagtgaagt	gacttgcgca	120
cacaaccagt	aaattggcag	agtcagattt	gaatccatgg	agtctggtct	gcactttcaa	180
tcaccgaata	ccctttctaa	gaaacgtgtg	ctgaatgagt	gcattggataa	atcagtgtct	240
actcaacatc	tttgctaga	tatccccgat	agacta			276

<210> 33
 <211> 477
 <212> DNA
 <213> Homo sapien

<400> 33
 tagtagttgc caaatatattg aaaattttacc cagaagtgat tgaaaacttt ttggaaacaa 60
 aaacaaataa agccaaaagg taaaataaaa atatctttgc actctcgta ttacctatcc 120
 ataacttttt caccgtaagc tctcctgctt gttagtgtag tgtgggtata ttaaactttt 180
 tagttattat tttttattca cttttccact agaaagtcac tattgattta gcacacatgt 240
 tgatctcatt tcattttttc tttttatagg caaaatttga tgctatgcaa caaaaatact 300
 caagcccatt atcttttttc cccccgaaat ctgaaaattg caggggacag aggggaagtta 360
 tcccattaaa aaattgtaaa tatgttcagt ttatgtttta aaatgcacaa aacataagaa 420
 aattgtgttt acttgagctg ctgattgtaa gcagttttat ctcaggggca actacta 477

<210> 34
 <211> 631
 <212> DNA
 <213> Homo sapien

<400> 34
 tagtagttgc caattcagat gatcagaaat gctgctttcc tcagcattgt cttgttaaac 60
 cgcattgccat ttggaacttt ggcagtgaga agccaaaagg aagagggtgaa tgacatatat 120
 atatatatat attcaatgaa agtaaaatgt atatgctcat atactttcta gttatcagaa 180
 tgagtttaagc tttatgccat tgggctgctg catattttta tcagaagata aaagaaaatc 240
 tgggcatttt tagaatgtga tacatgtttt tttaaaactg ttaaataatta tttcgatatt 300
 tgtctaagaa ccggaatgtt cttaaaattt actaaaacag tattgtttga ggaagagaaa 360
 actgtactgt ttgccattat tacagtgcga caagtgcag tcaagtcacc cactctctca 420
 ggcattcagta tccacctcat agctttacac attttgacgg ggaatattgc agcatcctca 480
 ggccctgacat ctgggaaagg ctcagatcca cctactgctc cttgctcggt gatttgtttt 540
 aaaatattgt gcctggtgtc acttttaagc cacagccctg cctaaaagcc agcagagaac 600
 agaaccgcga ccattctata ggcaactact a 631

<210> 35
 <211> 578
 <212> DNA
 <213> Homo sapien

<400> 35
 tagtagttgc catcccatat tacagaagge tctgtataca tgacttattt ggaagtgatc 60
 tgttttctct ccaaaccat ttatcgtaat ttcaccagtc ttggatcaat cttggtttcc 120
 actgatacca tgaaacctac ttggagcaga cattgcacag ttttctgtgg taaaaactaa 180
 aggtttattt gctaagctgt catcttatgc ttagtatttt ttttttacag tggggaattg 240
 ctgagattac attttggtat tcattagata ctttgggata acttgacact gtcttctttt 300
 tttcgctttt aattgctatc atcatgcttt tgaaacaaga acacattagt cctcaagtat 360
 tacataagct tgcttggtac gcctggtggt ttaaaggact atctttggcc tcagggtcac 420
 aagaatgggc aaagtgtttc cttatgttct gtagttctca ataaaagatt gccaggggcc 480
 gggtagctgt gctgcactg taatcccagc actttgggaa gctgaggctg gcggatcatg 540
 ttagggcagg tggtcgaaac cagcctgggc aactacta 578

<210> 36
 <211> 583
 <212> DNA
 <213> Homo sapien

<400> 36

tagtagttgc	ctgtaatccc	agcaactcag	gaggetgggg	caggagaatc	agttgaacct	60
gggaggcaga	agttgtaatt	agcaaagatc	gcaccattgc	acttcagcct	gggcaacaag	120
agtgagattc	catctcaaaa	acaaaaaaaa	gaaaaagaaa	agaaaaggaa	aaaacgtata	180
aaccagccca	aaacaaaatg	atcattcttt	taataagcaa	gactaattta	atgtgtttat	240
ttaatcaaag	cagttgaatc	ttctgagtta	ttgggtgaaa	tacccatgta	gttaatttag	300
ggttcttact	tgggtgaacg	tttgatgttc	acaggttata	aaatgggtta	caaggaaaat	360
gatgcataaa	gaatcttata	aactactaaa	aataaataaa	atataaatgg	ataggtgcta	420
tggatggagt	ttttgtgtaa	tttaaaatct	tgaagtcatt	ttggatgctc	attggttgctc	480
tggtaatctc	cattaggaaa	aggttatgat	atggggaaac	tgtttctgga	aattgcggaa	540
tgtttctcat	ctgtaaaatg	ctagtatctc	agggcaacta	cta		583

<210> 37

<211> 716

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(716)

<223> n = A,T,C or G

<400> 37

gatctactag	tcatntggat	tctatccatg	gcagctaagc	ctttctgaat	ggattctact	60
gctttcttgt	tctttaatcc	agacccttat	atatgtttat	gttcacaggc	agggcaatgt	120
ttagtgaaaa	caattctaaa	ttttttat	tgcattttca	tgctaatttc	cgtcacactc	180
cagcaggctt	cctgggagaa	taaggagaaa	tacagctaaa	gacattgtcc	ctgcttactt	240
acagccta	ggtatgcaaa	accacttcaa	taaagtaaca	ggaaaagtac	taaccaggta	300
gaatggacca	aaactgat	agaaaaatca	gaggaagaga	ggaacaaata	tttactgagt	360
cctagaatgt	acaaggcttt	ttaattacat	attttatgta	aggcctgcaa	aaaacagggtg	420
agtaatcaac	atgtgtccca	ttttacatat	aaggaaactg	aagcttaaat	tgaataat	480
aatgcataga	ttttatagtt	agaccatggt	cagggtcccta	tggtatactt	actagctgta	540
tgaatatgag	aaaataat	tggtattttc	ttggcatcag	tatttttcac	tgcaaaataa	600
agctaaagtt	atgtagcaaa	cagtcagcat	agtgcctgat	acatagtagg	tgctccaaac	660
atgattacnc	tantattngg	tattanaaaa	atccaatata	ggcntggata	aaaccg	716

<210> 38

<211> 688

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(688)

<223> n = A,T,C or G

<400> 38

ttctgtccac	atatcatccc	actttaattg	ttaatcagca	aaactttcaa	tgaaaaatca	60
tccattttta	ccaggatcac	accaggaaac	tgaagggtgta	ttttttttta	ccttaaaaaa	120
aaaaaaaaaa	accaaacaaa	ccaaaacaga	ttaacagcaa	agagttctaa	aaaatttaca	180
tttctcttac	aactgtcatt	cagagaacaa	tagttcttaa	gtctgttaaa	tcttggcatt	240
aacagagaaa	cttgatgaan	agttgtactt	ggaatattgt	ggattttttt	ttttgtctaa	300
tctcccccta	ttgttttgcc	aacagtaatt	taagtttggtg	tggaaacatcc	ccgtagttga	360
agtgtaaaca	atgtatagga	aggaatat	gataagatga	tgcatcacat	atgcattaca	420
tgtagggacc	ttcacaactt	catgcactca	gaaaacatgc	ttgaagagga	ggagaggacg	480

gcccaggggc	accatccagg	tgcccttgagg	acagagaatg	cagaagtggc	actgttgaaa	540
tttagaagac	catgtgtgaa	tggtttcagg	cctgggatgt	ttgccaccaa	gaagtgcctc	600
cgagaaattt	ctttcccatt	tggaatacac	ggtggcctga	tggttacggt	gggtgaccca	660
acgaagaaaa	tgaaattctg	ccctttcc				688

<210> 39

<211> 585

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(585)

<223> n = A,T,C or G

<400> 39

tagtagttgc	cgcnnaccta	aaanttggaa	agcatgatgt	ctaggaaaca	tantaaaata	60
gggtatgcct	atgtgtctaca	gagagatggt	agcattttaa	gtgcatantt	ttatgtattt	120
tgacaaatgc	atatnctct	ataatccaca	actgattacg	aagctattac	aattaaaaag	180
tttggccggg	cgtgggtggc	ggtggctgac	gcctgtaatc	ccagcacttt	gggaggccga	240
ggcacgcgga	tcacgaggtc	gggagttcaa	gaccatcctg	gctaacacgg	tgaaagtcca	300
tctctactaa	aaatacgaaa	aaattacccc	ggcgtgggtg	cgggcgccctg	tagtcccagc	360
tactccggag	gctgaggcag	gagaatggcg	tgaacccagg	acacggagct	tgacgtgtgc	420
caacatcacg	tactgcctc	ccagcctggg	ggacaggaac	aagantcccg	tcctcanaaa	480
agaaaaatac	tactnatant	ttcnacttta	ttttaantta	cacagaactn	cctcttggtg	540
cccccttacc	attcatctca	cccacctcct	atagggcacn	nctaa		585

<210> 40

<211> 475

<212> DNA

<213> Homo sapien

<400> 40

tctgtccaca	ccaatcttag	aagctctgaa	aagaatttgt	ctttaaatat	cttttaatat	60
taacatgtat	tttatggacc	aaattgacat	tttcgactgt	tttttccaaa	aaagtcagg	120
gaatttcagc	acactgagtt	gggaattttct	tatcccagaa	gaccaaccaa	tttcatattt	180
atttaagatt	gattccatac	tccgtttttca	aggagaatcc	ctgcagtctc	cttaaaggta	240
gaacaaatac	ttcctatttt	tttttcacca	ttgtgggatt	ggactttaag	aggtgactct	300
aaaaaaacag	agaacaaata	tgtctcagtt	gtattaagca	cggacccata	ttatcatatt	360
cacttaaaaa	aatgatttcc	tgtgcacctt	ttggcaactt	ctcttttcaa	tgtagggaaa	420
aacttagtca	ccctgaaaaac	ccacaaaata	aataaaaactt	gtagatgtgg	acaga	475

<210> 41

<211> 423

<212> DNA

<213> Homo sapien

<400> 41

taagagggtg	catcgggtaa	gaacgtaggc	acatctagag	cttagagaag	tctggggtag	60
gaaaaaaatc	taagtattta	taagggtata	ggtaacattt	aaaagtaggg	ctagctgaca	120
ttatttagaa	agaacacata	cggagagata	agggcaaaag	actaagacca	gaggaaact	180
aatatttagt	gatcacttcc	attcttggtg	aaaatagtaa	cttttaagtt	agcttcaagg	240
aagatttttg	gccatgatta	gttgtcaaaa	gttagttctc	ttgggtttat	attactaatt	300
ttgttttaag	atccttggtg	gtgctttaat	aaagtcatgt	tatatcaaac	gctctaaaac	360
attgtagcat	gttaaatgtc	acaatatact	taccatttgt	tgtatatggc	tgtaccctct	420

cta

423

<210> 42
 <211> 527
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(527)
 <223> n = A,T,C or G

<400> 42
 tctcctaggc taatgtgtgt gtttctgtaa aagtaaaaag ttaaaaattt taaaaataga 60
 aaaaagctta tagaataaga atatgaagaa agaaaatatt ttgtacatt tgcacaatga 120
 gtttatgttt taagctaagt gttattacaa aagagccaaa aaggttttta aaattaaaac 180
 gtttgtaaag ttacagtacc cttatgttaa ttataattg aagaaagaaa aacttttttt 240
 tataaatgta gtgtagccta agcatacagt atttataaag tctggcagtg ttcaataatg 300
 tcctaggcct tcacattcac tcaactgactc acccagagca acttccagtc ctgtaagctc 360
 cattcgtggt aagtgccta tacagggtgca ccatttattt tacagtattt ttactgtacc 420
 ttctctatgt ttccatatgt ttcgatatac aaataccact ggttactatn gcccnacagg 480
 taattccagt aacacggcct gtatacgtct ggtancccta gngaaga 527

<210> 43
 <211> 331
 <212> DNA
 <213> Homo sapien

<400> 43
 tcttcaacct cgtaggacaa ctctcatatg cctgggcact atttttaggt tactaccttg 60
 gctgcccttc ttttaagaaaa aaaaaagaag aaaaaagaac tttccacaa gtttctcttc 120
 ctctagttgg aaaattagag aaatcatgtt ttttaatttg tggtatttca gatcacaat 180
 tcaaacactt gtaaaccatta agcttctgtt caatcccttg ggaagaggat tcattctgat 240
 atttacgggt caaaagaagt tgtaatatgt tgcttggaac acagagaacc agttattaac 300
 ttcttactac tattatataa taaataataa c 331

<210> 44
 <211> 592
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(592)
 <223> n = A,T,C or G

<400> 44
 ggcttagtag ttgccaggca aaatarecgtt gattctcctc aggagccacc cccaacaccc 60
 ctgtttgctt ctagacctat acctagacta aagteccagc agacccttag aggtgaggtt 120
 cagagtgacc cttgaggaga tgtgctacac tagaaaagaa ctgcttgagt tttctaattt 180
 atataagcag aaatctggag aagagtcata ggaatggata ttaagggtgt gagataatgg 240
 cggaaggaat atagagttgg atcaggctgg acttattgat ttgaaccac taagtagaga 300
 ttctgctttt gatgttgag ctcagggtgt taaaaaagggt tttaatggtt ctaatagttt 360
 atttgcttgg ttagctgaaa tatggataaa agatggccca ctgtgagcaa gctggaaatg 420
 cctgatctct ctcagtttaa tgtagaggaa gggatccaaa agtttaggga ganttggtatg 480

ctggraktgg attggctact ttgrgacctt cccwtcccag ctgggagggg ccagaagata 540
cacccttgac caacgccttg cgaaatggat ttgtgatggc ggcaactact aa 592

<210> 45
<211> 567
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (567)
<223> n = A,T,C or G

<400> 45
ggcttagtag ttgccattgc gagtgcttgc tcaacgagcg ttgaacatgg cggattgtct 60
agattcaacg gatttgagtt ttaccagcaa agcgaaccaa gcgcggccca gagaattatg 120
ggttgggttg ctttgaaaag atggaaatcc tgtaggccta gtcagaaaag ccttcttgca 180
gaacagttgg ttctcgggcg aacgctcacc aagatgccca ttggaaaggc tagcgtgtat 240
ttgggagagc ctgatagcgt gtcttctgat gatgtttgtg cttggacagt gacaaaagat 300
atgcaaagca agtccgaact agacgtcaag cttcgtgagc aaattattgt agactcctac 360
ttatactgtg aggaatgata gccaaaggtg gggactttaaa gactaagggt gtttgtactt 420
gcgccgatga tcccaggcag aaagamctga tcgctagttt tatacgggca actactaagc 480
cgaattccag cacactggcg gccgttacta attggatccg anctcgggtac cagcttgatg 540
catascttga gttwtctata ntgtcnc 567

<210> 46
<211> 908
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (908)
<223> n = A,T,C or G

<400> 46
gagcgaagaa ccgagggcag ngnntangng cgangaagcg gagagggcca aaaagcaacc 60
gctttccccc gggggtgccg attcattaag gcaggtggag gacaggtttc ccgatggaag 120
gcggcagggg cgcaagcaat taatgtgagt aggccattca ttagcaccgg ggcttaacat 180
ttaagcttcg ggttggtatg tgggtgggaat tgtgagcgga taacaatttc acacaggaaa 240
cagctatgac catgattacg ccaagctatt taggtgacat tatagaataa ctcaagttat 300
gcatcaagct tggtagccag ttccggatcca ctagtaacgg ccgccagtgt gtggaattcg 360
gcttagtagt tgccgaccat ggagtgtctac ctaggctaga atacctgagy tctccctag 420
cctcactcac attaaattgt atcttttcta cattagatgt cctcagcgcc ttatttctgc 480
tggacwatcg ataaattaat cctgatagga ttagtagcag agattaatta ctgagagtat 540
gttaattgtt catccctcct atataacgta ttgtcatttt aatggagcaa ttctggagat 600
aatccctgaa ggcaaaggaa tgaatcttga ggggtgagaaa gccagaatca gtgtccagct 660
gcagttgttg gagaagggtg tattatgtat gtctcagaag tgacaccata tgggcaacta 720
ctaagcccga attccagcac actggcgggc gttactaatg gatccgagct cggtagcaag 780
cttgatgcat agcttgagta tctatagtgt cactaaatag cctggcggtt tcatgggtcat 840
agctgtttcc tgtgtgaaat tgttatccgc tcccaattcc cccaccata cgagccggaa 900
cataaagt 908

<210> 47
<211> 480

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(480)
<223> n = A,T,C or G

<400> 47
tgccaacaag gaaagtttta aatttcccct tgaggattct tggatgatcat caaattcagt 60
ggtttttaag gttgttttct gtcaaataac tctaacttta agccaaacag tatatggaag 120
cacagataka atattacaca gataaaagag gagttgatct aaagtaraga tagttggggg 180
ctttaatttc tggaacctag gtctcccat cttcttctgt gctgaggaac ttcttggaag 240
cggggattct aaagttcttt ggaagacagt ttgaaaacca ccatgttggt ctcagtacct 300
ttatttttaa aaagtaggtg aacattttga gagagaaaag ggcttggtg agatgaagtc 360
ccccccccc cttttttttt ttttagctga aatagatacc ctatgttnaa rgaarggatt 420
attatttacc atgccaytar scacatgctc tttgatgggc nytccestac cctccttaag 480

<210> 48
<211> 591
<212> DNA
<213> Homo sapien

<400> 48
aagaggggtac cgagtggaaat ttccgcttca ctagtctggt gtggctagtc ggtttcgtgg 60
tggccaacat tacgaacttc caactcaacc gttcttggtgac gttcaagcgg gagtaccggc 120
gaggatgggtg gcgtgaattc tggcctttct ttgccgtggg atcggtagcc gccatcatcg 180
gtatgtttat caagatcttc tttactaacc cgacctctcc gatttacctg cccgagccgt 240
ggtttaacga ggggaggggg atccagtcac gcgagtactg gtcccagatc ttccgcatcg 300
tcgtgacaat gcctatcaac ttcgctcgta ataagttgtg gaccttccga acggtgaagc 360
actccgaaaa cgtccggtgg ctgctgtgct gtgactccca aaatcttgat aacaacaagg 420
taaccgaatc gcgctaagga accccggcat ctccgggtact ctgcatatgc gtaccoccta 480
agccgaattc cagcacactg gcggccgtta ctaattggat ccgaactccg taaccaagcc 540
tgatgcgtaa cttgagttat tctatagtgt ccctaaaata acctggcggt a 591

<210> 49
<211> 454
<212> DNA
<213> Homo sapien

<400> 49
aagaggggtac ctgccttgaa atttaaattgt ctaaggaaar tgggagatga ttaagagttg 60
gtgtggcyta gtcacaccaa aatgtattta ttacatcctg ctcccttcta gttgacagga 120
aagaaagctg ctgtggggaa aggagggata aatactgaag ggatttacta aacaaatgtc 180
catcacagag ttttcccttt tttttttttg agacagagtc ttgctctgtc acccaggctg 240
gaatgaagwg gtatgatctc agttgaatgc aacctctacc tcctagggtc aagcgattct 300
catgcctcag cctcctgagc agctgggact ataggcgcat gctaccatgc caggctaatt 360
tttatatttt tattagagac ggggtgttgc catgttggcc aggcaggtct cgaactcctg 420
ggcctcagat gatctgcccc accgtaccct ctta 454

<210> 50
<211> 463
<212> DNA
<213> Homo sapien

<400> 50
aagaggggtac caaaaaaaaag aaaaaggaaa aaaagaaaaa caacttgtat aaggctttct 60
gctgcataca gctttttttt tttaaataaa tgggtgccaac aaatgttttt gcattcacac 120
caattgctgg ttttgaaatc gtactcttca aaggatattg tgcagatcaa tccaatagtg 180
atgccccgta gggtttgtgg actgcccacg ttgtctacct tctcatgtag gagccattga 240
gagactgttt ggacatgcct gtgttcatgt agccgtgatg tccgggggcc gtgtacatca 300
tggtaccgtg ggggtggggtc tgcattggct gctgggcata tggctgggtg cccatcatgc 360
ccatctgcat ctgcataggg tattggggcg tttgatccat atagccatga ttgctgtggt 420
agccactgtt catcattggc tgggacatgc tggtaccctc tta 463

<210> 51
<211> 399
<212> DNA
<213> Homo sapien

<400> 51
cttcaacctc ccaaagtgtc gggattacag gactgagcca ccacgctcag cctaagcctc 60
tttttacta ccctctaagc gatctaccac agtgatgagg ggctaaagag cagtgcattt 120
tgattacaat aatggaactt agatttatta attaacaatt tttccttagc atgttggttc 180
cataattatt aagagtatgg acttacttag aaatgagctt tcattttaag aatttcattc 240
ttgaccttct ctattagtct gagcagtatg acactatacg tattttattt aactaaccta 300
ccttgagcta ttacttttta aaaggctata tacatgaatg tgtattgtca actgtaaagc 360
cccacagtat ttaattatat catgatgtct ttgagggtg 399

<210> 52
<211> 392
<212> DNA
<213> Homo sapien

<400> 52
cttcaacctc aatcaacctt ggtaattgat aaaatcatca cttaactttc tgatataatg 60
gcaataatta tctgagaaaa aaaagtgggtg aaagattaaa cttgcatttc tctcagaatc 120
ttgaaggata tttgaataat tcaaaagcgg atccagtatg atcagccgaa gaaactcact 180
tagctagaac gttggaccga tggatctaaag tccctgccct tccactaacc agctgattgg 240
ttttgtgtaa acctcctaca cgcttgggct tggctgcctc atttgtcaaa gtaaaggctg 300
aaataggaag ataatgaacc gtgtcttttt ggtctctttt ccatccatta ctctgatttt 360
acaaagaggg ctgtattccc ctgggtgagg tg 392

<210> 53
<211> 179
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (179)
<223> n = A,T,C or G

<400> 53
ttcgggtgat gcctcctcag gctacagtga agactggatt acagaaagggt gccagcgaga 60
tttcagattc ctgtaaacct ctaaagaaaa ggagtcgcgc ctcaactgat gttagaatga 120
ctagttcagc atacngagac acntctgact ccgattctag aggactgagt gacctgcan 179

<210> 54
<211> 112

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(112)
<223> n = A,T,C or G

<400> 54
ttcgggtgat gcctcctcag gctacatcat natagaagca aagtagaana atcnngtttg 60
tgcattttcc cacanacaaa attcaaata ntggaagaaa ttggganagt at 112

<210> 55
<211> 225
<212> DNA
<213> Homo sapien

<400> 55
tgagcttccg cttctgacaa ctcaatagat aatcaaagga caactttaac agggattcac 60
aaaggagtat atccaaatgc caataaacat ataaaaagga attcagcttc atcatcatca 120
gaagwatgca aattaaaacc ataatagagaa accactatgt ccactagaa tagataaaat 180
cttaaaagac tggtaaaacc aagtgttggt aaggcaagag gagca 225

<210> 56
<211> 175
<212> DNA
<213> Homo sapien

<400> 56
gctcctcttg ccttaccac acattctcaa aaacctgtta gagtcctaag cattctcctg 60
ttagtattgg gattttaccc ctgtcctata aagatgttat gtacaaaaaa tgaagtggag 120
ggccataccc tgagggaggg gagggatctc tagtgttgtc agaagcggaa gctca 175

<210> 57
<211> 223
<212> DNA
<213> Homo sapien

<400> 57
agccatttac cacccatgga tgaatggatt ttgtaattct agctgttgta ttttgtgaat 60
ttgttaattt tgttgttttt ctgtgaaaca catacattgg atatgggagg taaaggagtg 120
tcccagttgc tcttggtcac tccctttata gccattactg tcttgtttct tgtaactcag 180
gttaggtttt ggtctctctt gctccactgc aaaaaaaaaa aaa 223

<210> 58
<211> 211
<212> DNA
<213> Homo sapien

<400> 58
gttcgaaggt gaacgtgtag gtagcggatc tcacaactgg ggaactgtca aagacgaatt 60
aactgacttg gatcaatcaa atgtgactga ggaaacacct gaaggtgaag aacatcatcc 120
agtggcagac actgaaaata aggagaatga agttgaagag gtaaaagagg aggggtccaa 180
agagatgact ttggatgggt ggtaaatggc t 211

<210> 59
 <211> 208
 <212> DNA
 <213> Homo sapien

<400> 59
 gctcctcttg ccttaccaac tttgcaccca tcatcaacca tgtggccagg tttgcagccc 60
 aggctgcaca tcaggggact gcctcgcaat acttcatgct gttgctgctg actgatgggtg
 120ctgtgacgga tgtggaagcc acacgtgagg ctgtgggtgcg tgctcgaaac ctgcccattgt
 180
 cagtgatcat tatgggtggt aaatggct 208

<210> 60
 <211> 171
 <212> DNA
 <213> Homo sapien

<400> 60
 agccatttac caccataact aaattctagt tcaaactcca acttcttcca taaaacatct 60
 aaccactgac accagttggc aatagcttct tccttcttta acctcttaga gtatttatgg 120
 tcaatgccac acatttctgc aactgaataa agttggtgtaag gcaagaggag c 171

<210> 61
 <211> 134
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (134)
 <223> n = A,T,C or G

<400> 61
 cgggtgatgc ctcctcaggc tttggtgtgt ccactcnact cactggcctc ttctccagca 60
 actggtgaan atgtcctcan gaaaancncc acacgcngct caggggtgggg tgggaancat 120
 canaatcatc nggc 134

<210> 62
 <211> 145
 <212> DNA
 <213> Homo sapien

<400> 62
 agaggggtaca tatgcaacag tatataaagg aagaagtgca ctgagaggaa cttcatcaag 60
 gccatttaat caataagtga tagagtcaag gctcaaccca ggtgtgacgg attccaggtc 120
 ccaagctcct tactggtacc ctctt 145

<210> 63
 <211> 297
 <212> DNA
 <213> Homo sapien

<400> 63
 tgcactgaga ggaattcaaa gggtttatgc caaagaacaa accagtcctc tgcagcctaa 60
 ctcatttgtt tttgggctgc gaagccatgt agagggcgat caggcagtag atggtccttc 120

ccacagtcag	cgccatggtg	gtccggtaaa	gcatttggtc	aggcaggcct	cgtttcaggt	180
agacgggcac	acatcagctt	tctggaaaa	ctttttagtc	tctggagctt	tgtttttccc	240
agcataatca	tacactgtgg	aatcggaggt	cagtttagtt	ggtaaggcaa	gaggagc	297

<210> 64

<211> 300

<212> DNA

<213> Homo sapien

<400> 64

gcactgagag	gaacttccaa	tactatgttg	aataggagtg	gtgagagagg	gcattccttgt	60
cttgtgccgg	ttttcaaagg	gaatgcttcc	agcttttgcc	cattcagtat	aatattaaag	120
aatgttttac	cattttctgt	cttgccctgtt	tttctgtgtt	tttgttggtc	tcttcattct	180
ccatttttag	gcctttacat	gttaggaata	tatttctttt	aatgatactt	cacctttggt	240
atcttttgtg	agactctact	catagtgtga	taagcactgg	gttggttaagg	caagaggagc	300

<210> 65

<211> 203

<212> DNA

<213> Homo sapien

<400> 65

gctcctcttg	ccttaccaac	tcaccagta	tgtcagcaat	tttatcrget	ttacctacga	60
aacagcctgt	atccaaacac	ttaacacact	cacctgaaaa	gttcaggcaa	caatcgctt	120
ctcatgggtc	tctctgtctc	agttctgaac	ctttctcttt	tcctagaaca	tgcatttarg	180
tcgatagaag	ttcctctcag	tgc				203

<210> 66

<211> 344

<212> DNA

<213> Homo sapien

<400> 66

tacgggggacc	cctgcattga	gaaagcgaga	ctcactctga	agctgaaatg	ctgttgccct	60
tgcagtgctg	gtagcaggag	ttctgtgctt	tgtgggctaa	ggctcctgga	tgacccctga	120
catggagaag	gcagagtgtg	gtgcccttc	tcatggctc	gtcaaggcat	catggactgc	180
cacacacaaa	atgccgtttt	tattaacgac	atgaaattga	aggagagaac	acaattcact	240
gatgtggctc	gtaaccatgg	atatggtcac	atacagaggt	gtgattatgt	aaagggtaat	300
tccaccacc	tcattgtggaa	actagcctca	atgcaggggt	ccca		344

<210> 67

<211> 157

<212> DNA

<213> Homo sapien

<400> 67

gcactgagag	gaacttcgta	gggaggttga	actggctgct	gaggaggggg	aacaacaggg	60
taaccagact	gatagccatt	ggatggataa	tatgggtggt	gaggagggac	actacttata	120
gcagaggggt	gtgtatagcc	tgaggaggca	tcaccg			157

<210> 68

<211> 137

<212> DNA

<213> Homo sapien

<400> 68
gcactgagag gaacttctag aaagtgaaag tctagacata aaataaaaata aaaattttaa 60
actcaggaga gacagcccag cacggtggct cacgcctgta atcccagaac tttgggagcc 120
tgaggaggca tcacccg 137

<210> 69
<211> 137
<212> DNA
<213> Homo sapien

<400> 69
cgggtgatgc ctctcaggc tgtatatttga agactatcga ctggacttct tatcaactga 60
agaatccgtt aaaaatacca gttgtattat ttctacctgt caaaatccat ttcaaagtgt 120
gaagttcttc tcagtgc 137

<210> 70
<211> 220
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (220)
<223> n = A,T,C or G

<400> 70
agcatgttga gccagacac gcaatctgaa tgagtgtgca cctcaagtaa atgtctacac 60
gctgcctggt ctgacatggc acaccatcnc gtggagggca casctctgct cngcctacwa 120
cgagggcant ctcattwgaca gggtccaccc accaaactgc aagaggctca nnaagtactr 180
ccaggggtmya sggacmasgg tgggaytyca ycacwcatct 220

<210> 71
<211> 353
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (353)
<223> n = A,T,C or G

<400> 71
cgtaggggtc tctatccact gctaaacct acacctgggt aaacaggac catttaacat 60
tccanctaa atatgccaag tgacttcaca tgtttatctt aaagatgtcc aaaacgcaac 120
tgattttctc ccctaaacct gtgatgggtg gatgattaan cctgagtgggt ctacagcaag 180
ttaagtgcaa ggtgctaaat gaangtgacc tgagatacag catctacaag gcagtacctc 240
tcaacncagg gcaactttgc ttctcanagg gcatttagca gtgtctgaag taatttctgt 300
attacaactc acggggcggg ggggtgaatat ctantggana gnagacccta acg 353

<210> 72
<211> 343
<212> DNA
<213> Homo sapien

<400> 72

gcactgagag	gaacttccaa	tacyatkac	agagtgaaca	rgcarccyac	agaacaggag	60
aaaatgttyg	caatctctcc	atctgacaaa	aggctaatat	ccagawtcta	awaggaactt	120
aaacaaattt	atgagaaaag	aacaracaac	ctcawcaaaa	agtgggtgaa	ggawatgcts	180
aaargaagac	atytattcag	ccagtaaaca	yatgaaaaaa	aggctcatsa	tcactgawca	240
ttagagaaat	gcaaatcaaa	accacaatga	gataccatct	yayrccagtr	agaaygggtga	300
tcattaaaaar	stcaggaaac	aacagatgct	ggacaagggtg	tca		343

<210> 73
 <211> 321
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (321)
 <223> n = A,T,C or G

<400> 73						
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agaaggtgag	aaagtctttg	gttctgaagc	agcttctaag	atcttttcat	ttgcttcatt	120
tcaaagttcc	catgctgcca	aagtgccatc	ctttggggta	ctgttttctg	agctccagtg	180
ataactcatt	tatacaaggg	agatacccag	aaaaaaagtg	agcaaattctt	aaaaaggtgg	240
cttgagttca	gccttaaata	ccatcttgaa	atgacacaga	gaaagaanga	tggtgggtgg	300
gagtggatag	agaccctaac	g				321

<210> 74
 <211> 321
 <212> DNA
 <213> Homo sapien

<400> 74						
gcactgagag	gaacttcaga	gagagagaga	gagttccacc	ctgtacttgg	ggagagaaac	60
agaaggtgag	aaagtctttg	gttctgaagc	agcttctaag	atcttttcat	ttgcttcatt	120
tcaaagttcc	catgctgcca	aagtgccatc	ctttggggta	ctgttttctg	agctccagtg	180
ataactcatt	tatacaaggg	agatacccag	aaaaaaagtg	agcaaattctt	aaaaaggtgg	240
cttgagttca	gycttaaata	ccatcttgaa	atgamacaga	gaaagaagga	tggtgggtgg	300
gagtggatag	agaccctaac	g				321

<210> 75
 <211> 317
 <212> DNA
 <213> Homo sapien

<400> 75						
gcactgagag	gaacttccac	atgcactgag	aaatgcatgt	tcacaaggac	tgaagtctgg	60
aactcagttt	ctcagttcca	atcctgattc	aggtgtttac	cagctacaca	accttaagca	120
agtcagataa	ccttagcttc	ctcatatgca	aaatgagaat	gaaaagtact	catcgctgaa	180
ttgttttgag	gattagaaaa	acatctggca	tgtagtagaa	attcaattag	tattcatttt	240
cattcttcta	aattaaacaa	ataggatttt	tagtggtgga	acttcagaca	ccagaaatgg	300
gagtggatag	agaccct					317

<210> 76
 <211> 244
 <212> DNA
 <213> Homo sapien

<400> 76
 cgttagggtc tctatccact cccactactg atcaaactct atttatttaa ttatttttat 60
 catactttaa gttctgggat acacgtgcag catgcgcagg tttgttgcag aggtatacac 120
 ttgccatggt ggtttgctgc acccatcagt ccatcatcta cattaggtat ttctcctaata 180
 gctatccctc cccatagcccc ttacaccccc aacaggctct agtgtgtgaa gttcctctca 240
 gtgc 244

<210> 77
 <211> 254
 <212> DNA
 <213> Homo sapien

<400> 77
 cgttagggtc tctatccact gaaatctgaa gcacaggagg aagagaagca gtyctagtga 60
 gatggcaagt tcttttacca cactctttaa catttygttt agttttaacc tttatttatg 120
 gataataaag gttaataatta ataatgattt attttaaggc attcccraat ttgcataatt 180
 ctcccttttg agataccctt ttatctccag tgcaagtctg gatcaaagtg atasamagaa 240
 gttcctctca gtgc 254

<210> 78
 <211> 355
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(355)
 <223> n = A,T,C or G

<400> 78
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 ccggtatggc acgaagacgc actgganac gtgcttacgt ccttttgctc tgttgatggc 120
 cctgagggga cgcaggaccc ttatgacctt cagaatcttc acaacgggag atggcactgg 180
 attgantccc antgacacca gagacacccc aaccaccagn atatcantat attgatgtag 240
 ttctgtaga nggccccctt gtggaggaaa gctccatnag ttggtcatct tcaacaggat 300
 ctcaacagtt tccgatggct gtgatgggca tagtcatant taacntgtn tcgaa 355

<210> 79
 <211> 406
 <212> DNA
 <213> Homo sapien

<400> 79
 taagagggtg ccagcagaaa ggtagtagtc atcagatagc atcttatacg agtaatatgc 60
 ctgctatttg aagtgttaatt gagaaggaaa atttttagct gctcactgac ctgctgtag 120
 ccccagtgac agctaggatg tgcattctcc agccatcaag agactgagtc aagttgttcc 180
 ttaagtcaga acagcagact cagctctgac attctgattc gaatgacact gttcaggaat 240
 cggaatcctg tctgattagac tggacagctt gtggcaagtg aatttgctg taacaagcca 300
 gattttttta aatttatatt gtaaataatg tgtgtgtgtg tgtgtgtata tatatatata 360
 tgtacagtta tctaagttaa tttaaaagtt gtttggtacc ctctta 406

<210> 80
 <211> 327
 <212> DNA

<213> Homo sapien

<400> 80

tttttttttt	tttactcggc	tcagtcta	cctttttgta	gtcactcata	ggccagactt	60
agggctagga	tgatgattaa	taagagggat	gacataacta	ttagtggcag	gtagttgtt	120
tgtagggctc	atggtagggg	taaaaggagg	gcaatttcta	gatcaaataa	taagaaggta	180
atagctacta	agaagaattt	tatggagaaa	gggacgcggg	cgggggatat	agggtcgaag	240
ccgcactcgt	aaggggtgga	tttttctatg	tagccgttga	gttgtggtag	tcaaaatgta	300
ataattatta	gtagtaagcc	taggaga				327

<210> 81

<211> 318

<212> DNA

<213> Homo sapien

<400> 81

tagtctatgc	ggttgattcg	gcaatccatt	atttgctgga	ttttgtcatg	tgttttgcca	60
attgcattca	taatttatta	tgcatTTatg	cttgtatctc	ctaagtcatg	gtatataatc	120
catgcttttt	atgTTTTgtc	tgacataaac	tcttatcaga	gccctttgca	cacagggatt	180
caataaatat	taacacagtc	tacatttatt	tggtgaatat	tgcatatctg	ctgtactgaa	240
agcacattaa	gtaacaaagg	caagtgagaa	gaatgaaaag	cactactcac	aacagttatc	300
atgattgcgc	atagacta					318

<210> 82

<211> 338

<212> DNA

<213> Homo sapien

<400> 82

tcttcaacct	ctactccac	taatagcttt	ttgatgactt	ctagcaagcc	tcgctaacct	60
cgccttacc	cccactatta	acctactggg	agaactctct	gtgctagtaa	ccacgttctc	120
ctgatcaaat	atcactctcc	tacttacagg	actcaacata	ctagtccacag	ccctatactc	180
cctctacata	tttaccacaa	cacaatgggg	ctcactcacc	caccacatta	acaacataaa	240
accctcattc	acacgagaaa	acaccctcat	gttcatacac	ctatccccca	ttctctctct	300
atccctcaac	cccgcacatca	ttaccgggtt	ttcctctt			338

<210> 83

<211> 111

<212> DNA

<213> Homo sapien

<400> 83

agccattttac	cacccatcca	caaaaaaaaa	aaaaaaaaaag	aaaaatatca	aggaataaaa	60
atagacttttg	aacaaaaagg	aacattttgct	ggcctgagga	ggcatcacc	g	111

<210> 84

<211> 224

<212> DNA

<213> Homo sapien

<400> 84

tcgggtgatg	cctcctcagg	ccaagaagat	aaagcttcag	acccctaaca	catttccaaa	60
aaggaagaaa	ggagaaaaaa	gggcatcatc	ccggttcoga	agggtcaggg	aggaggaaat	120
tgagggtggat	tcacgagttg	cggacaactc	ctttgatgcc	aagcgaggtg	cagccgggaga	180
ctggggagag	cgagccaatc	aggttttgaa	gttcctctca	gtgc		224

<210> 85
<211> 348
<212> DNA
<213> Homo sapien

<400> 85
gcactgagag gaacttcggt ggaaacgggt ttttttcatg taaggctaga cagaagaatt 60
ctcagtaact tccttggtgt gtgtgtattc aactcacasa gttgaacgat cctttacaca 120
gagcagactt gtaacactct twttgtggaa ttgcaagtg gagatttcag scgctttgaa 180
gtsaaaggta gaaaaggaaa tatcttccta taaaaactag acagaatgat tctcagaaac 240
tcctttgtga tgtgtgcgtt caactcacag agtttaacct ttcwtttcat agaagcagtt 300
aggaaacact ctgtttgtaa agtctgcaag tggatagaga ccctaacg 348

<210> 86
<211> 293
<212> DNA
<213> Homo sapien

<400> 86
gcactgagag gaacttcytc gtgwtgktg yattcaactc acagagttga asswtsmttt 60
acabagwkca ggcttkcaaa cactcttttt gtmgatytg caagwggaka tttsrrccrc 120
tttgwggycw wysktmgaaw mgyrwtatc ttcwyatmra amctagacag aaksattctc 180
akaawstyry ytgtgawgs tgcrttcaac tcacagagkt kaacmwtyct kytsatrgag 240
cagttwkgaa actctmtttc ttgggattct gcaagtggat agagacccta acg 293

<210> 87
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 87 10
ctcctaggct

<210> 88
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 88 10
agtagttgcc

<210> 89
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 89
ttccggttatg c 11

<210> 90
<211> 10
<212> DNA
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 90
tggtaaaggg 10

<210> 91
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 91
tcggtcatag 10

<210> 92
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 92
tacaacgagg 10

<210> 93
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 93
tggattggtc 10

<210> 94
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
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<400> 94	
ctttctaccc	10
<210> 95	
<211> 10	
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<220>	
<223> Primer for amplification from breast tumor cDNA	
<400> 95	
ttttggctcc	10
<210> 96	
<211> 10	
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<400> 96	
ggaaccaatc	10
<210> 97	
<211> 10	
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<400> 97	
tcgatacagg	10
<210> 98	
<211> 10	
<212> DNA	
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<223> Primer for amplification from breast tumor cDNA	
<400> 98	
ggtactaagg	10
<210> 99	
<211> 10	
<212> DNA	
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<220>	
<223> Primer for amplification from breast tumor cDNA	

<400> 99
agtctatgcg 10

<210> 100
<211> 10
<212> DNA
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 100
ctatccatgg 10

<210> 101
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 101
tctgtccaca 10

<210> 102
<211> 10
<212> DNA
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<220>
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<400> 102
aagagggtac 10

<210> 103
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 103
cttcaacctc 10

<210> 104
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 104
gctcctcttg ccttaccaac 20

<210> 105
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 105
gtaagtcgag cagtgtgatg 20

<210> 106
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 106
gtaagtcgag cagtctgatg 20

<210> 107
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 107
gacttagtgg aaagaatgta 20

<210> 108
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 108
gtaattccgc caaccgtagt 20

<210> 109
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 109
atggttgatc gatagtggaa 20

<210> 110
<211> 20
<212> DNA
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 110
acgggggaccc ctgcattgag 20

<210> 111
<211> 20
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<220>
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<400> 111
tattctagac cattcgctac 20

<210> 112
<211> 20
<212> DNA
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<220>
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<400> 112
acataaccac ttttagcgttc 20

<210> 113
<211> 20
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<220>
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<400> 113
cggggtgatgc ctcttcaggc 20

<210> 114
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<400> 114 20
agcatgttga gccagacac

<210> 115
<211> 20
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<400> 115 20
gacaccttgt ccagcatctg

<210> 116
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<400> 116 20
tacgctgcaa cactgtggag

<210> 117
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<220>
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<400> 117 20
cgttagggtc tctatccact

<210> 118
<211> 20
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 118 20
agactgactc atgtccccta

<210> 119
<211> 20
<212> DNA
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 119
tcatcgctcg gtgactcaag 20

<210> 120
<211> 20
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<220>
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<400> 120
caagattcca taggctgacc 20

<210> 121
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 121
acgtactggc cttgaaggtc 20

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 122
gacgcttgga cacttgacac 20

<210> 123
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 123
gtatcgacgt agtggctctcc 20

<210> 124
<211> 20
<212> DNA
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 124
tagtgacatt acgacgctgg 20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 125
cgggtgatgc ctctcaggc 20

<210> 126
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 126
atggctatatt tcgggggctg aca 23

<210> 127
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 127
ccggtatctc ctctgggta tt 22

<210> 128
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 128
ctgcctgagc cacaaatg 18

<210> 129
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 129
ccggaggagg aagctagagg aata

24

<210> 130
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 130
tttttttttt ttag

14

<210> 131
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited Th Motifs (B-cell epitopes)

<400> 131
Ser Ser Gly Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val
1 5 10 15
Gly Ile

<210> 132
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited Th Motifs (B-cell epitopes)

<221> VARIANT
<222> (1)...(22)
<223> Xaa = Any Amino Acid

<400> 132
Gln Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Xaa Ile Glu Val
1 5 10 15
Val Gln Gly His Asp Glu
20

<210> 133
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited Th Motifs (B-cell epitopes)

<400> 133
Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu Ala Tyr Arg Ile Tyr
1 5 10 15
Thr Pro Phe Asp Leu Ser Ala
20

<210> 134
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 134
Tyr Leu Leu Val Gly Ile Gln Gly Ala
1 5

<210> 135
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 135
Gly Ala Ala Gln Lys Pro Ile Asn Leu
1 5

<210> 136
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<221> VARIANT
<222> (1)...(9)
<223> Xaa = Any Amino Acid

<400> 136
Asn Leu Ser Lys Xaa Ile Glu Val Val
1 5

<210> 137
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 137

Glu Val Val Gln Gly His Asp Glu Ser
1 5

<210> 138
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 138
His Leu Gln Glu Ala Tyr Arg Ile Tyr
1 5

<210> 139
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 139
Asn Leu Ala Phe Val Ala Gln Ala Ala
1 5

<210> 140
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 140
Phe Val Ala Gln Ala Ala Pro Asp Ser
1 5

<210> 141
<211> 9388
<212> DNA
<213> Homo sapien

<400> 141
gctcgcggcc gcgagctcaa ttaaccctca ctaaagggag tcgactcgat cagactgtta 60
ctgtgtctat gtagaaagaa gtagacataa gagattccat tttgttctgt actaagaaaa 120
attcttctgc cttgagatgc tgtaaatctg taaccctagc cccaaccctg tgctcacaga 180
gacatgtgct gtgttgactc aaggttcaat ggatttaggg ctatgctttg ttaaaaaagt 240
gcttgaagat aatatgcttg ttaaaagtca tcaccattct ctaatctcaa gtaccagg 300
acacaataca ctgcggaagg ccgcagggac ctctgtctag gaaagccagg tattgtccaa 360
gatttctccc catgtgatag cctgagatat ggctcatgg gaagggttaag acctgactgt 420
ccccagccc gacatcccc agcccgacat cccccagccc gacacccgaa aagggtctgt 480
gctgaggagg attagtaaaa gaggaaggcc tctttgcagt tgaggtaaga ggaaggcatc 540
tgtctcctgc tcgtccctgg gcaatagaat gtcttggtgt aaaaccgat tgtatgttct 600

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<210> 142

<211> 419

<212> DNA

<213> Homo sapien

<400> 142

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<210> 143

<211> 402

<212> DNA

<213> Homo sapien

<400> 143

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<211> 224

<212> DNA

<213> Homo sapien

<400> 144

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<210> 145

<211> 111

<212> DNA

<213> Homo sapien

<400> 145

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<210> 146

<211> 585

<212> DNA

<213> Homo sapien

<400> 146

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<210> 147

<211> 579

<212> DNA

<213> Homo sapien

<220>

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<222> (1) ... (579)

<223> n = A,T,C or G

<400> 147

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<210> 148

<211> 249

<212> DNA

<213> Homo sapien

<400> 148

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<210> 149

<211> 255

<212> DNA

<213> Homo sapien

<400> 149

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<210> 150

<211> 318

<212> DNA

<213> Homo sapien

<400> 150

ttacgctgca	acactgtgga	ggccaagctg	ggatcacttc	ttcattctaa	ctggagagga	60
gggaagtcca	agtccagcag	aggggtgggtg	ggtagacagt	ggcactcaga	aatgtcagct	120
ggacccctgt	ccccgcatag	gcaggacagc	aaggctgtgg	ctctccaggg	ccagctgaag	180
aacaggacac	tgtctccgct	gccacaaagc	gtcagagact	cccatctttg	aagcacggcc	240
ttcttgggtc	tcctgcactt	ccctgttctg	ttagagacct	ggttatagac	aaggtttctc	300
cacagtgttg	cagcgtaa					318

<210> 151

<211> 323

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(323)

<223> n = A,T,C or G

<400> 151tnacgcngcn acnntgtaga ganggnaagg cnttccccac attnccccctt
catnanagaa 60
ttattcnacc aagnntgacc natgccttt atgacttaca tgcnnactnc ntaatctgtg 120
tcnngcctta aaagcnntc cactacatgc ntcancactg tntgtgtnac ntcatnaact 180
gtcngnaata ggggcncata actacagaaa tgcanttcac actgcttcca ntgccatcng 240
cgtgtggcct tncctactct tcttntattc caagtagcat ctctggantg cttccccact 300
ctccacattg ttgcagcnat aat 323

<210> 152

<211> 311

<212> DNA

<213> Homo sapien

<400> 152
tcaagattcc ataggctgac cagtccaagg agagttgaaa tcatgaagga gagtctatct 60
ggagagagct gtagttttga gggttgcaaa gacttaggat ggagttggtg ggtgtgggta 120
gtctctaagg ttgattttgt tcataaattt catgccctga atgccttgct tgcctcacc 180
tggtccaagc cttagtgaac acctaaaagt ctctgtcttc ttgctctcca aacttctcct 240
gaggatttcc tcagattgtc tacattcaga tcgaagccag ttggcaaaca agatgcagtc 300
cagagggtca g 311

<210> 153

<211> 332

<212> DNA

<213> Homo sapien

<400> 153
caagattcca taggctgacc aggaggctat tcaagatctc tggcagttga ggaagtctct 60
ttaagaaaat agtttaaaac atttgtaaaa atttttctgt cttacttcat ttctgtagca 120
gttgatatct ggctgtcctt tttataatgc agagtgggaa ctttcctac catgtttgat 180
aaatgttgtc caggctccat tgccaataat gtgttggtcca aaatgcctgt ttagttttta 240
aagacggaac tccacccttt gcttggtctt aagtatgtat ggaatgttat gataggacat 300
agtagtagcg gtggtcagcc tatggaatct tg 332

<210> 154

<211> 345

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(345)

<223> n = A,T,C or G

<400> 154
tcaagattcc ataggctgac ctggacagag atctcctggg tctggcccag gacagcaggc 60
tcaagctcag tggagaaggt ttccatgacc ctcagattcc cccaaacctt ggattgggtg 120
acattgcac tcctcagaga gggaggagat gtangtctgg gcttccacag ggacctggta 180

ttttaggatc aggggtaccgc tggcctgagg cttggatcat tcanagcctg ggggtggaat 240
ggctggcagc ctgtggcccc attgaaatag gctctggggc actccctctg ttcctanttg 300
aacttgggta aggaacagga atgtgggtcan cctatggaat cttga 345

<210> 155
<211> 295
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (295)
<223> n = A,T,C or G

<400> 155
gacgcttggc cacttgacac attaaacagt tttgcataat cactancatg tattttctagt 60
ttgctgtctg ctgtgatgcc ctgccctgat tctctggcgt taatgatggc aagcataatc 120
aaacgctgtt ctgttaattc caagttataa ctggcattga ttaaagcatt atctttcaca 180
actaaactgt tcttcatana acagcccata ttattatcaa attaagagac aatgtattcc 240
aatatccttt anggccaata tatttnatgt cccttaatta agagctactg tccgt 295

<210> 156
<211> 406
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (406)
<223> n = A,T,C or G

<400> 156
gacgcttggc cacttgacac tgcagtggga aaaccagcat gagccgctgc cccaaggaa 60
cctcgaagcc caggcagagg accagccatc ccagcctgca ggtaaagtgt gtcacctgtc 120
aggtgggctt ggggtgagtg ggtgggggaa gtgtgtgtgc aaagggggtg tnaatgtnta 180
tgcgtgtgag catgagtgat ggctagtgtg actgcatgtc agggagtgtg aacaagcgtg 240
cgggggtgtg tgtgcaagtg cgtatgcata tgagaatatg tgtctgtgga tgagtgcatt 300
tgaaagtctg tgtgtgtgcg tgtggtcatg anggtaantt antgactgcg caggatgtgt 360
gagtgtgcat ggaacactca ntgtgtgtgt caagtggccn ancgtc 406

<210> 157
<211> 208
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (208)
<223> n = A,T,C or G

<400> 157
tgacgcttgg ccacttgaca cactaaaggg tgttactcat cactttcttc tctcctcggt 60
ggcatgtgag tgcattctatt cacttggcac tcatttgttt ggcagtgact gtaanccana 120
tctgatgcat acaccagctt gtaaattgaa taaatgtctc taatactatg tgctcacaat 180
anggtanggg tgaggagaag gggagaga 208

<210> 158
 <211> 547
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(547)
 <223> n = A,T,C or G

<400> 158
 cttcaacctc cttcaacctc cttcaacctc ctggattcaa acaatcatcc cacctcagac 60
 tccttagtag ctgagactac agactcacgc cactacatct ggctaaattt ttgtagagat 120
 agggtttcat catgttgccc tggctgggtct caaactcctg acctcaagca atgtgcccac 180
 ctcagcctcc caaagtgtct ggattacagg cataagccac catgcccagt ccatntttaa 240
 tctttcctac cacattctta ccacactttc ttttatgttt agatacataa atgcttacca 300
 ttatgataca attgcccaca gtattaagac agtaacatgc tgcacagggt tgtagcctag 360
 gaacagtagg caataccaca tagcttaggt gtgtggtaga ctataccatc taggtttgtg 420
 taagtacac tttatgtctgt ttacacaatg aaaaaccat ctaatgatgc atttctcaga 480
 atgtatcctt gtcagtaagc tatgatgtac agggaacact gccaaggac acagatattg 540
 tacctgt 547

<210> 159
 <211> 203
 <212> DNA
 <213> Homo sapien

<400> 159
 gctcctcttg cettaccaac tcacccagta tgtcagcaat tttatcrgct ttacctacga 60
 aacagcctgt atccaaacac ttaacacact cacctgaaaa gttcaggcaa caatcgctt 120
 ctcattgggtc tctctgtctc agttctgaac ctttctcttt tctagaaca tgcatttarg 180
 tcgatagaag ttcctctcag tgc 203

<210> 160
 <211> 402
 <212> DNA
 <213> Homo sapien

<400> 160
 tgtaagtcca gcagtgtgat ggggtggaaca ggggtgtaag cagtaattgc aaactgtatt 60
 taaacaataa taataatatt tagcatttat agagcacttt atatcttcaa agtacttgca 120
 aacattayct aattaaatac cctctctgat tataatctgg atacaaatgc acttaaaactc 180
 aggacagggt catgagaraa gtatgcattt gaaagttggt gctagctatg ctttaaaaac 240
 ctatacaatg atgggraagt tagagttcag attctgttgg actgtttttg tgcatttcag 300
 ttcagcctga tggcagaatt agatcatatc tgcactcgat gactygtgct gataacttat 360
 cactgaaatc tgagtgttga tcatcacact gctcgactta ca 402

<210> 161
 <211> 193
 <212> DNA
 <213> Homo sapien

<400> 161
 agcatgttga gccagacac tgaccaggag aaaaaccaac caatagaaac acgcccagac 60

actgaccagg agaaaaacca accaataaaa acaggcccg acataagaca aataataaaa 120
 ttagcggaca aggacatgaa aacagctatt gtaagagcgg atatagtgggt gtgtgtctgg 180
 gctcaacatg cta 193

<210> 162
 <211> 147
 <212> DNA
 <213> Homo sapien

<400> 162
 tgttgagccc agacactgac caggagaaaa accaaccaat aaaaacaggc ccggacataa 60
 gacaaataat aaaattagcg gacaaggaca tgaaaacagc tattgtaaga gcggatatag 120
 tgggtgtgtgt ctgggctcaa catgcta 147

<210> 163
 <211> 294
 <212> DNA
 <213> Homo sapien

<400> 163
 tagcatgttg agcccagaca caaatctttc cttaagcaat aaatcatttc tgcataatgtt 60
 tttaaaacca cagctaagcc atgattattc aaaaggacta ttgtattggg tattttgatt 120
 tgggtttctta tctccctcac attatcttca tttctatcat tgacctctta tcccagagac 180
 tctcaaaactt ttatgttata caaatcacat tctgtctcaa aaaatatctc acccacttct 240
 cttctgtttc tgcgtgtgta tgtgtgtgtg tgtgtgtctg ggctcaacat gcta 294

<210> 164
 <211> 412
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(412)
 <223> n = A,T,C or G

<400> 164
 cgggattggc tttgagctgc agatgctgcc tgtgaccgca cccggcgtgg aacagaaagc 60
 cacctggctg caagtgcgcc agagccgccc tgactacgtg ctgctgtggg gctggggcgt 120
 gatgaactcc accgccctga aggaagccca ggccaccgga taccctcgcg acaagatgta 180
 cggcgtgtgg tgggcccgtg cggagcccga tgtgctgtgac gtgggcgaag gcgccaaggg 240
 ctacaacgcg ctggctctga acggctacgg cacgcagtc aaggtgatcc angacatcct 300
 gaaacacgtg cacgacaagg gccagggcac ggggcccaaa gacgaagtgg gctcgggtgct 360
 gtacacccgc ggcgtgatca tccagatgct ggacaagggtg tcaatcacta at 412

<210> 165
 <211> 361
 <212> DNA
 <213> Homo sapien

<400> 165
 ttgacacctt gtccagcatc tgcattctgat gagagcctca gatggctacc actaatggca 60
 gaaggcaaaag gagaacaggc attgtatggc aagaaaggaa gaaagagaga ggggagaaaag 120
 gtgctaggtt cttttcaaca accagttctt gatggaactg agagtaagag ctcaaggcca 180
 ggtgtggtga ctccaaccag taatcccaac attttaggag gctgaggcag gcagatgtct 240

```

tgaccccatg agtttgtgac cagcctgaac aacatcatga gactccatct ctacaataat      300
tacaaaaaatt aatcaggcat tgtggtatgc cctgtagtcc cagatgctgg acaagggtgc      360
a                                          361

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<210> 166
<211> 427
<212> DNA
<213> Homo sapien

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<400> 166
twgactgact catgtcccct acacccaact atcttctcca ggtggccagg catgatagaa      60
tctgatcctg acttagggga atattttctt ttacttccc atcttgattc cctgccggtg      120
agtttcctgg ttcagggtaa gaaaggagct caggccaaag taatgaacaa atccatcctc      180
acagacgtac agaataagag aacwtggacw tagccagcag aacmcaaktg aaamcagaac      240
mcttamctag gatracaamc merraratar ktgcycmcmc wtataataga aaccaaactt      300
gtatctaatt aaatatttat ccacygtcag ggcatttagt gttttgataa atacgctttg      360
gctaggattc ctgaggttag aatggaaraa caattgcamc gagggtaggg gacatgagtc      420
aktctaa                                          427

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<210> 167
<211> 500
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(500)
<223> n = A,T,C or G

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<400> 167
aacgtcgcat gctcccgcc gccatggccg cgggatagac tgactcatgt cccctaagat      60
agaggagaca cctgctaggt gtaaggagaa gatggttagg tctacggagg ctccagggtg      120
ggagtagttc cctgctaagg gagggtagac tgttcaacct gttcctgctc cggcctccac      180
tatagcagat gcgagcagga gtaggagaga gggaggtaag agtcagaagc ttatgttggt      240
tatgcgggga aacgcrrtat cgggggcagc cragttatta ggggacantr tagwyartcw      300
agntagcatc caaagcgngg gagtntccc atatggttgg acctgcaggc ggccgcatta      360
gtgattagca tctgagcccc agacacgcat agcaacaagg acctaaactc agatcctgtg      420
ctgattactt aacatgaatt attgtattta ttaacaact ttgagttatg aggcataatta      480
ttaggtccat attacctgga                                          500

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```

<210> 168
<211> 358
<212> DNA
<213> Homo sapien

```

```

<400> 168
ttcatcgctc ggtgactcaa gcctgtaatc ccagaacttt gggaggccga ggggagcaga      60
tcacctgagg ttgggagttt gagaccagcc tggccaacat ggtgacaacc cgtctctgct      120
aaaaatacaa aaattagcca agcatggtgg catgcacttg taatcccagc tactcgggag      180
gctgaggcag gagaatcact tgaggccagg aggcagaggt tgcagtgagg cagaggttga      240
gatcatgcca ctgcactcca gcctgggcaa cagagtaaga ctccatctca aaaaaaaaaa      300
aaaaaaagaa tgatcagagc caaaaatata gaaaaccttg agtcaccgag cgatgaaa      358

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<210> 169
<211> 1265

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<212> DNA

<213> Homo sapien

<400> 169

ttctgtccac	accaatctta	gagctctgaa	agaatttgtc	tttaaataac	ttttaatagt	60
aacatgtatt	ttatggacca	aattgacatt	ttcgactatt	ttttcccaaa	aaaagtcagg	120
tgaatttcag	cacactgagt	tgggaatttc	ttatcccaga	agwccgcacg	agcaatttca	180
tatttattta	agattgattc	catactccgt	tttcaaggag	aatccctgca	gtctccttaa	240
aggtagaaca	aatactttct	atTTTTTTTT	caccattgtg	ggattggact	ttaagagggtg	300
actctaaaaa	aacagagAAC	aaatatgtct	cagttgtatt	aagcacggac	ccatattatc	360
atattcactt	aaaaaaatga	tttctgtgtc	accttttggc	aacttctctt	ttcaatgtag	420
ggaaaaactt	agtcaccctg	aaaaccacac	aaataaataa	aacttgtaga	tgtgggcaga	480
argtttgggg	gtggacattg	tatgtgttta	aattaaaccc	tgtatcactg	agaagctggt	540
gtatgggtca	gagaaaatga	atgcttagaa	gctgttcaca	tcttcaagag	cagaagcaaa	600
ccacatgtct	cagctatatt	attattttatt	ttttatgcat	aaagtgaatc	atctcttctg	660
tattaatttc	caaagggttt	tacctcttat	ttaaatgctt	tgaaaaacag	tgcattgaca	720
atgggttgat	atTTTTtctt	aaaagaaaaa	tataattatg	aaagccaaga	taatctgaag	780
cctgttttat	tttaaaactt	tttatgttct	gtgggtgatg	ttgtttgttt	gtttgtttct	840
atTTTgttgg	ttttttactt	tgttttttgt	tttgttttgt	tttggtttdg	catactacat	900
gcagtttctt	taaccaatgt	ctgtttggtc	aatgtaatta	aagttgttaa	tttatatgag	960
tgcatttcaa	ctatgttcaat	ggtttcttaa	tatttattgt	gtagaagtac	tggtaatTTT	1020
tttatttaca	atatgtttaa	agagataaca	gtttgatatg	ttttcatgtg	tttatagcag	1080
aagttatttta	tttctatggc	attccagcgg	atattttggg	gtttgcgagg	catgcagtca	1140
atatttttga	cagttagtgg	acagtattca	gcaacgcctg	atagcttctt	tggccttatg	1200
ttaaataaaa	agacctgttt	gggatgtaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1260
aaaaaa						1265

<210> 170

<211> 383

<212> DNA

<213> Homo sapien

<400> 170

tgtaagtcca	gcagtgtgat	gacgatattc	ttcttattaa	tgtggtaatt	gaacaaatga	60
tctgtgatac	tgatcctgag	ctaggaggcg	ctgttcagtt	aatgggactt	cttcgtactc	120
taattgatcc	agagaacatg	ctggctacaa	ctaataaaac	cgaaaaaagt	gaattttctaa	180
atTTTTtcta	caaccattgt	atgcattgtt	tcacagcacc	acttttgacc	aatacttcag	240
aagacaaatg	tgaaaaggat	aatatagtgt	gatcaaacaa	aaacaacaca	atTTTgtccc	300
ataattatca	aacagcacag	ctacttgctt	taatttttaga	gttactcaca	ttttgtgtgg	360
aacatcacac	tgctcgactt	aca				383

<210> 171

<211> 383

<212> DNA

<213> Homo sapien

<400> 171

tgggcacctt	caatatcgca	agttaaaaat	aatgttgagt	ttattatact	tttgacctgt	60
ttagtccaac	agggtgaagg	catgtaaaga	atgtggactt	ctgagggaatt	ttctttttaa	120
aagaacataa	tgaagtaaca	ttttaattac	tcaaggacta	cttttggttg	aagtttataa	180
tctagatacc	tctacttttt	gtttttgctg	ttcgacagtt	cacaaagacc	ttcagcaatt	240
tacagggtaa	aatcgttgaa	gtagtggagg	tgaaactgaa	attttaaatt	attctgtaaa	300
tactataggg	aaagaggctg	agcttagaat	cttttggttg	ttcatgtgtt	ctgtgctctt	360
atcatcacac	tgctcgactt	aca				383

<210> 172
 <211> 699
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(699)
 <223> n = A,T,C or G

<400> 172
 tcgggtgatg cctcctcagg cttgtcggtta gtgtacacag agctgctcat gaagcgacag 60
 cggctgcccc tggcaattca gaacctcttc ctctacactt ttggtgcgct tctgaatcta 120
 ggtctgcatg ctggcggcgg ctctggccca ggctcctgg aaagtctctc aggatgggca 180
 gcactcgtgg tgetgagcca ggcactaaat ggactgctca tgtctgctgt catggagcat 240
 ggcagcagca tcacacgcct ctttgtggtg tcttgctcgc tgggtggtaa cgccgtgctc 300
 tcagcagtc tgctacggct gcagctcaca gccgccttct tcttggccac attgctcatt 360
 ggcctggcca tgcgcctgta ctatggcagc cgctagtccc tgacaacttc caccctgatt 420
 ccggaccctg tagattgggc gccaccacca gatccccctc ccaggccttc ctccctctcc 480
 catcagcggc cctgtaacaa gtgccttggtg agaaaagctg gagaagtgaag ggcagccagg 540
 ttattctctg gaggttggtg gatgaagggg tacccttagg agatgtgaag tgtgggttg 600
 gttaaggaaa tgcttaccat cccccacccc caaccaagtt nttccagact aaagaattaa 660
 ggtaacatca atacctaggc ctgaggaggc atcaccoga 699

<210> 173
 <211> 701
 <212> DNA
 <213> Homo sapien

<400> 173
 tcgggtgatg cctcctcagg ccagatcaaa cttgggggttg aaaactgtgc aaagaaatca 60
 atgtcggaga aagaattttg caaaagaaaa atgcctaata agtactaatt taataggtca 120
 cattagcagt ggaagaagaa atgttgatat tttatgtcag ctattttata atcaccagag 180
 tgcttagctt catgtaagcc atctcgtatt cattagaaat aagaacaatt ttattcgtcg 240
 gaaagaactt ttcaatttat agcatcttaa ttgtcagga ttttaaattt tgataaagaa 300
 agctccactt ttggcaggag tagggggcag ggagagagga ggctccatcc acaaggacag 360
 agacaccagg gccagtagg tagctgggtg ctggatcagt cacaacggac tgacttatgc 420
 catgagaaga aacaacctcc aaatctcagt tgcttaatac aacacaagct ctttcttgc 480
 tcacggtaca tgtcctatgt agatcaacag cagggtgactc agggaccag gctccatctc 540
 catatgagct tccatagtca ccaggacacg ggctctgaaa gtgtcctcca tgcagggaca 600
 catgcctctt cctttcattg ggcagagcaa gtcacttatg gccagaagtc aactgcagg 660
 gcagtgccat cctgctgtat gcctgaggag gcacacccc a 701

<210> 174
 <211> 700
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(700)
 <223> n = A,T,C or G

<400> 174
 tcgggtgatg cctcctcagg cccctaaatc agagtccagg gtcagagcca caggagacag 60

ggaaagacat	agattttaac	cggccccctt	caggagattc	tgaggctcag	ttcactttgt	120
tgcaagttga	acagaggcag	caaggctagt	ggtagggggc	acggtctcta	aagctgcact	180
gcctggatct	gcctcccagc	tctgccagga	accagctgcg	tggccttgag	ctgctgacac	240
gcagaaagcc	ccctgtggac	ccagtctcct	cgtctgtaag	atgaggacag	gact.ctagga	300
accctttccc	ttggtttggc	ctcactttca	caggctccca	tcttgaactc	tatctactct	360
tttctgaaa	ccttgtaaaa	gaaaaaagt	ctagcctggg	caacatggca	aaaccctgtc	420
tctacaaaa	atacaaaaat	tagttgggtg	tgggtggcatg	tgctgtagt	cccagccact	480
tgggaggtgc	tgaggtggga	ggatcacttg	agcccgagg	gtggaggttg	cagtgaagca	540
agatcatgcc	actgcactcc	agcctgagta	atagagtaag	actctgtctc	aaaaacaaca	600
acaacaacag	tgagtgtgcc	tctgtttccg	ggttggtggg	ggcaccacat	ttatgcatct	660
ctcagatttg	gacgtgcag	cctgaggagg	catcacccga			700

<210> 175

<211> 484

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (484)

<223> n = A,T,C or G

<400> 175						60
tatagggcga	attgggccc	agttgcatgn	tcccggccgc	catggccgcg	ggattcgggt	120
gatgcctcct	caggcttggt	tgccacaagc	tacttctctg	agctcagaaa	gtgccccttg	180
atgagggaaa	atgtcctact	gcactgcgaa	tttctcagtt	ccattttacc	tcccagtcct	240
ccttctaatac	cagttaataa	attcattcca	caagtattta	ctgattacct	gcttgtgcca	300
gggactattc	tcaggctgaa	gaaggtggga	ggggagggcg	gaacctgagg	agccacctga	360
gccagcttta	tatttcaacc	atggctggcc	catctgagag	catctcccca	ctctcgccaa	420
cctatcgggg	catagcccag	ggatgcccc	aggcgcccca	ggtagatgc	gtccctttgg	480
cttgtcagtg	atgacataca	ccttagctgc	ttagctgggtg	ctggcctgag	gaggcatcac	484
ccga						

<210> 176

<211> 432

<212> DNA

<213> Homo sapien

<400> 176						60
tcgggtgatg	cctcctcagg	gctcaaggga	tgagaagtga	cttctttctg	gagggaccgt	120
tcatgccacc	caggatgaaa	atggataggg	acccacttgg	aggacttgct	gatatgtttg	180
gacaaatgcc	aggtagcgga	attggtactg	gtccaggagt	tatccaggat	agattttcac	240
ccaccatggg	acgtcatcgt	tcaaatcaac	tcttcaatgg	ccatggggga	cacatcatgc	300
ctccacacac	atcgagttt	ggagagatgg	gaggcaagtt	tatgaaaagc	caggggctaa	360
gccagctcta	ccataaccag	agtcagggac	tcttatccca	gctgcaagga	cagtcgaagg	420
atatgccacc	tcggttttct	aagaaaggac	agcttaatgc	agatgagatt	agcctgagga	432
ggcatcacc	ga					

<210> 177

<211> 788

<212> DNA

<213> Homo sapien

<400> 177						60
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catgctggag	ccaagtgeta	acatgccttg	gttcaagggg	tggaaagtca	cccgttaagga	120
tggcaatgcc	agtggaaacca	cgtgtcttga	ggctctggac	tgcacccctac	caccaactcg	180
cccaactgac	aagcccttgc	gcctgcctct	ccaggatgtc	tacaaaattg	gtggtattgg	240
tactgttccct	gttggccgag	tggagactgg	tgttctcaaa	cccggtatgg	tggtcacctt	300
tgctccagtc	aacgtttacaa	cggaagtaaa	atctgtcgaa	atgcaccatg	aagctttgag	360
tgaagctctt	cctggggaca	atgtgggctt	caatgtcaag	aatgtgtctg	tcaaggatgt	420
tcgtcgtggc	aacgtttgctg	gtgacagcaa	aaatgaccca	ccaatggaag	cagctggctt	480
cactgctcag	gtgattatcc	tgaaccatcc	aggccaaata	agtgcgggct	atgcccctgt	540
attggattgc	cacacggctc	acattgcatg	caagtttgc	gagctgaagg	aaaagattga	600
tcgccgttct	ggtaaaaagc	tggaagatgg	ccctaaattc	ttgaagtctg	gtgatgctgc	660
cattgttgat	atggttctctg	gcaagcccat	gtgtgttgag	agcttctcag	actatccacc	720
tttgggtcgc	tttgctgttc	gtgatatgag	acagacagtt	gcggtgggtg	tctgggctca	780
acatgcta						788

<210> 178
 <211> 786
 <212> DNA
 <213> Homo sapien

<400> 178						
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cacttgggct	gcactttgaa	tgacacactt	ggctttatta	gattcactag	tttttaaaaa	120
attgtttgtc	gtttcttttc	attaaagggt	taatcagaca	gatcagacag	cataattttg	180
tatttaatga	cagaaacgtt	ggtacatttc	ttcatgaatg	agcttgcatt	ctgaagcaag	240
agcctacaaa	aggcacttgt	tataaatgaa	agttctggct	ctagaggcca	gtactctgga	300
gtttcagagc	agccagtgat	tgttccagtc	agtgatgcct	agttatatag	aggaggagta	360
cactgtgcac	tcttctaggt	gtaagggtat	gcaactttgg	atcttaaaat	tctgtacaca	420
tacacacttt	atatatatgt	atgtatgtat	gaaaacatga	aattagtttg	tcaaatatgt	480
gtgtgtttag	tatttttagct	tagtgcaact	atttccacat	tatttattaa	attgatctaa	540
gacactttct	tgttgacacc	ttgaatatta	atgttcaagg	gtgcaatgtg	tattccttta	600
gattgttaaa	gcttaattac	tatgatttgt	agtaaattaa	cttttaaaat	gtatttgagc	660
ccttctgtag	tgctgtaggg	ctcttacagg	gtgggaaaga	ttttaatttt	ccagttgcta	720
attgaacagt	atggcctcat	tatatatttt	gatttatagg	agtttgtgtc	tgggctcaac	780
atgcta						786

<210> 179
 <211> 796
 <212> DNA
 <213> Homo sapien

<400> 179						
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gcttttaaaa	agccagtga	cctttttaat	actttggcaa	ccttctttca	caggcaaaga	120
acacccccat	ccgccccttg	tttggagtgc	agagtttggc	tttggttctt	tgccttgect	180
ggagtatact	tctaattcct	gttgctctgc	acaagctgaa	taccgagcta	cccaccgcca	240
cccaggccag	gtttccactc	atattattact	ttatgtttct	gttccattgc	tggteccacag	300
aaataagttt	tcctttggag	gaatgtgatt	ataccctttt	aatttctctc	ttttgctttt	360
ttttaatatc	attggtatgt	gtttggccca	gaggaaactg	aaattcacca	tcattctgac	420
tggcaatccc	attaccatgc	tttttttaaa	aaacgtaatt	tttcttgect	tacattggca	480
gagtagccct	tcctggctac	tggcttaatg	tagtcaacta	gtttctaggt	ggcattaggg	540
atgagacctg	aagcacagac	tgtctttacca	caaaagggtga	caagatctca	aaccttagcc	600
aaaggcctat	gtcaggtttc	aatgctatct	gcttctgttc	ctgctcactg	ttctggattt	660
tgctccttct	catccctagc	accagaattt	cccagttctc	ctccctacct	tccctgtttt	720
taattctaat	ctatcagcaa	aataactttt	caaagtgttt	aaccggtatc	tccatgtgtc	780
tgggctcaac	atgcta					796

<210> 180
 <211> 488
 <212> DNA
 <213> Homo sapien

<400> 180
 ggatgtgctg caaggcgatt aagttgggta acgccagggg tttcccagtc acgacgttgt 60
 aaaacgacgg ccagtgaatt gtaatacgac tcactatagg gcgaattggg cccgacgtcg 120
 catgctcccg gccgccatgg ccgcgggata gcatgttgag cccagacacc tgcagggtcat 180
 ttggagagat ttttcacgtt accagcttga tggctctttt caggaggaga gacactgagc 240
 actcccaagg tgagggtgaa gatttcctct agatagccgg ataagaagac taggagggat 300
 gectagaaaa tgattagcat gcaaatttct acctgccatt tcagaactgt gtgtcagccc 360
 acattcagct gcttcttgtg aactgaaaag agagaggtat tgagactttt ctgatggccg 420
 ctctaacatt gtaacacagt aatctgtgtg tgtgtgggtg tgtgtgtgtg tctgggctca 480
 acatgcta 488

<210> 181
 <211> 317
 <212> DNA
 <213> Homo sapien

<400> 181
 tagcatgttg agcccagaca cggcgacggg acctgatgag tgggggtgatg gcacctgtga 60
 aaaggaggaa cgtcatcccc catgatattg gggaccagga tgatgaacca tggctccgcg 120
 tcaatgcata tttaatccat gatactgctg attggaagga cctgaacctg aagtttgtgc 180
 tgcaggttta tcgggactat tacctcacgg gtgatcaaaa ctctctgaag gacatgtggc 240
 ctgtgtgtct agtaagggat gcacatgcag tggccagtgt gccaggggta tggttggtgt 300
 ctgggctcaa catgcta 317

<210> 182
 <211> 507
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(507)
 <223> n = A,T,C or G

<400> 182
 tagcatgttg agcccagaca ctggctgtta gccaaatcct ctctcagctg ctccctgtgg 60
 tttggtgact caggattaca gaggcacccg gtttcaggga acaaaaagat tttagctgcc 120
 agcagagagc accacataca ttagaatggg aaggactgcc acctccttca agaacaggag 180
 tgagggtggt ggtgaatggg aatggaagcc tgcattccct gatgcatttg tgctctctca 240
 aatcctgtct tagtcttagg aaaggaagta aagtttcaag gacgggtccg aactgctttt 300
 tgtgtctggg ctcaacatgc tatcccgcgg ccattggcggc cgggagcatg cgacgtcggg 360
 cccaattcgc cctatagtga gtcgtattac aattcactgg ccgtcgtttt acaacgtcgt 420
 gactgggaaa accctggcgt taccacaactt aatgccttg cagcacatcc ccctttccca 480
 gctggcgtaa tancgaaaag gcccgca 507

<210> 183
 <211> 227
 <212> DNA
 <213> Homo sapien

<400> 183
 gatttacgct gcaacactgt ggaggtagcc ctggagcaag gcaggcatgg atgcttctgc 60
 aatccccaaa tggagcctgg tatttcagcc aggaatctga gcagagcccc ctctaattgt 120
 agcaatgata agttattctc tttgttcttc aaccttccaa tagccttgag cttccagggg 180
 agtgtcgta atcattacag cctgggtctcc acagtgttgc agcgtaa 227

<210> 184
 <211> 225
 <212> DNA
 <213> Homo sapien

<400> 184
 ttacgctgca acactgtgga gcagattaac atcagacttt tctatcaaca tgactgggggt 60
 tactaaaaag acaacaaatc aatggcttca aaagtctaag gaataatttc gatacttcaa 120
 ctttataaaa cctgacaaaa ctatcaatca agcataaaga cagatgaaga acatttccag 180
 attttggcca atcagatatt ttacctccac agtggtgcag cgtaa 225

<210> 185
 <211> 597
 <212> DNA
 <213> Homo sapien

<400> 185
 ggcccgaagt cgcattgtcc cggccgccat ggccgcggga ttcgttaggg tctctatcca 60
 ctgggaccca taggctagtc agagtattta gagttgagtt cctttctgct tcccagaatt 120
 tgaaagaaaa ggagtgaggt gatagagctg agagatcaga tttgcctctg aagcctgttc 180
 aagatgtatg tgctcagacc ccaccactgg ggcctgtggg tgaggtcctg ggcattctatt 240
 tgaatgaatt gctgaagggg agcactatgc caaggaaggg gaacccatcc tggcactggc 300
 acaggggtca ccttatccag tgctcagtc ttctttgctg ctacctggtt ttctctcata 360
 tgtgaggggc aggtaagaag aagtgccrg tgttgtgcga gttttagaac atctaccagt 420
 aagtggggaa gtttcacaaa gcagcagctt tgttttgtgt attttcacct tcagttagaa 480
 gaggaaggct gtgagatgaa tgttagttga gtggaaaaga cgggtaagct tagtgatag 540
 agaccctaac gaatcactag tgcggccgcc ttgcaggctg accatatggg agagctc 597

<210> 186
 <211> 597
 <212> DNA
 <213> Homo sapien

<400> 186
 ggcccgaagt tgcattgtcc cggccgccat ggccgcggga ttcgttaggg tctctatcca 60
 ctacctaaaa aatcccaaac atataactga actcctcaca cccaattgga ccaatccatc 120
 accccagagg cctacagatc ctcccttgat acataagaaa atttcccaa actacctaac 180
 tatatcattt tgcaagattt gttttaccaa attttgatgg cctttctgag cttgtcagtg 240
 tgaaccacta ttacgaacga tcggatatta actgcccctc accgtccagg tgtagctggc 300
 aacatcaagt gcagtaaata ttcattaagt ttccacctac taagggtgctt aaacacccta 360
 ggggtgccatg tcggtagcag atcttttgat ttgtttttat ttcccataag ggtcctgttc 420
 aaggtcaatc atacatgtag tgtgagcagc tagtcactat cgcattgact ggagggtgat 480
 aatagaggcc tcctttgctg ttaaagaact cttgtcccag cctgtcaaag tggatagaga 540
 ccctaacgaa tcactagtgc ggccgcctgc aggtcgacca tatgggagag ctcccaa 597

<210> 187
 <211> 324
 <212> DNA

<213> Homo sapien

<400> 187

tcgttagggg	ctctatccac	ttgcaggtaa	aatccaatcc	tgtgtatata	ttatagtctt	60
ccatatgtag	tggttcaaga	gactgcagtt	ccagaaagac	tagccgagcc	catccatgtc	120
ttccacttaa	ccctgctttg	ggttacacat	cttaactttt	ctgttcaagt	ttctctgtgt	180
agtttatagc	atgagtattg	ggawaatgcc	ctgaaacctg	acatgagatc	tgggaaacac	240
aaacttactc	aataagaatt	tctcccatat	ttttatgatg	gaaaaatttc	acatgcacag	300
aggagtggat	agagacccta	acga				324

<210> 188

<211> 178

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(178)

<223> n = A,T,C or G

<400> 188

gcgcggggat	tcgggggtgat	acctcctcat	gccaaaatac	aacgtntaat	ttcacaactt	60
gccttccaat	ttacgcattt	tcaatttgct	ctccccattt	gttgagtcac	aacaaacacc	120
attgcccgaga	aacatgtatt	acctaacatg	cacatactct	taaaactact	catccctt	178

<210> 189

<211> 367

<212> DNA

<213> Homo sapien

<400> 189

tgacaccttg	tccagcatct	gacacagtct	tggctcttgg	aaaatattgg	ataaatgaaa	60
atgaatttct	ttagcaagtg	gtataagctg	agaatatacg	tatcacatat	cctcattcta	120
agacacattc	agtgtccctg	aaattagaat	aggacttaca	ataagtgtgt	tcactttctc	180
aatagctgtt	attcaattga	tggtaggcct	taaaagtcaa	agaaatgaga	gggcatgtga	240
aaaaaagctc	aacatcactg	atcattagaa	aacttccatt	caaaccacca	atgagatacc	300
atctcatacc	agtcagaatg	gctattatta	aaaagtcaaa	aaataacaga	tgctggacaa	360
ggtgtca						367

<210> 190

<211> 369

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(369)

<223> n = A,T,C or G

<400> 190

gacaccttgt	ccagcatctg	acaacgctaa	cagcctgagg	agatctttat	ttatttattt	60
agtttttact	ctggctaggg	agatgggtgg	taaaacattc	atttaccat	ttattcattt	120
aattgttcct	gcaaggccta	tggatagagt	attgtccagc	actgctctgg	aagctaggag	180
catgggggat	aacaagatag	gctacatcct	gttcccacag	aacttccact	ttagtctggg	240
aaacagatga	tatatacaaa	tatataaatg	aattcaggta	gttttaagta	cgaaaagaat	300

aagaaagcag agtcatgatt tanaatgctg gaaacagggg ctattgcttg agatattgaa 360
ggtgcccaa 369

<210> 191
<211> 369
<212> DNA
<213> Homo sapien

<400> 191
tgacaccttg tccagcatct gcacagggaa aagaaactat tatcagagtg aacaggcaac 60
ctacagaatg ggagaaaatt tttgcaatct atccatctga caaagggcta atatccagaa 120
tctacaaaga acttatacaa atttacaaga aacaaacaaa caaacaactc ctcaaaaagt 180
gggtgaagga tgtgaacaga cactttctcaa aagaagacat ttatggggcc aacaaacata 240
tgaaaaaaag ctcatcatca ctggtcacta gataaatgca aatcaaaacc acaatgagat 300
accatctcat tccagttaga atggcaatca ttaaaaagtc aggaaacaac agatgctgga 360
caaggtgctc 369

<210> 192
<211> 449
<212> DNA
<213> Homo sapien

<400> 192
tgacgcttgg ccacttgaca cttcatcttt gcacagaaaa acttctttac agattttaatt 60
caagactggg ctagtgacag tcctccagac attttttcat ttgttccata tacgtggaat 120
tttaaaatca tgtttcatca gtttgaaatg atttgggctg ctaatcaaca caattggatc 180
gactgttcta ctaaacaaca ggaaaatgtg tatctggcag cctgtggaga aacactaaac 240
attgattttt ctttgccttt tacggacttt gttccagcta catgtaatac caagttctct 300
ttaagaggag aagatgttga tcttcatttg tttctaccag actgccacc tagtaaatat 360
tctttattta tgctggtaaa aaattgccat ccaaataaga tgattcatga tactggtatt 420
cctgctgagt gtcaagtggc caagcgtca 449

<210> 193
<211> 372
<212> DNA
<213> Homo sapien

<400> 193
tgacgcttgg ccacttgaca ccagggatgt akcagttgaa tataatcctg caattgtaca 60
tattggcaat ttcccatcaa acattctaga aagagacaac caggattgct aggccataaa 120
agctgcaata aataactggt aattgcagta atcatttcag gccattcaa tccagtttgg 180
ctcagaggtg cctttggctg agagaagagg tgagatataa tgtgttttct tgcaacttct 240
tggaagaata actccacaat agtctgagga ctagatacaa acctatttgc cattaagca 300
ccagagtctg ttaattccag tactgataag tgttgagat tagactccag tgtgtcaagt 360
ggccaagcgt ca 372

<210> 194
<211> 309
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (309)
<223> n = A,T,C or G

<400> 194
 tgacgcttgg ccacttgaca cttatgtaga atccatcgtg ggctgatgca agccctttat 60
 ttaggcttag tggtgtgggc accttcaata tcacactaga gacaaacgcc acaagatctg 120
 cagaaacatt cagttctgan cactcgaatg gcaggataac tttttgtgtt gtaatccttc 180
 acatatacaa aaacaaactc tgcantctca cgttacaaaa aaacgtactg ctgtaaaata 240
 ttaagaaggg gtaaaggata ccactataa caaagtaact tacaactagt gtcaagtggc 300
 caagcgtca 309

<210> 195
 <211> 312
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(312)
 <223> n = A,T,C or G

<400> 195
 tgacgcttgg ccacttgaca cccaatctcg cacttcatcc tcccagcacc tgatgaagta 60
 ggactgcaac tatccccact tcccagatga ggggaccaan gtacacatta ggaccggat 120
 gggagcacag atttgtccga tcccagactc caagcactca gcgtcactcc aggacagcgg 180
 ctttcagata aggtcacaaa catgaatggc tccgacaacc ggagtcagtc cgtgctgagt 240
 taaggcaatg gtgacacgga tgcacgtgtn acctgtaatg gttcatcgta agtgtcaagt 300
 ggccaagcgt ca 312

<210> 196
 <211> 288
 <212> DNA
 <213> Homo sapien

<400> 196
 tgtatcgacg tagtgggtctc ctcagccatg cagaactgtg actcaattaa acctctttcc 60
 tttatgaatt acccaatctc gggtagtgtc tttatagtag tgtgagaatg gactaataca 120
 agtacatttt acttagtaat aataataaac aaatatatta catttttgtg tatttactac 180
 accatatttt ttattgttat tgtagtgtac accttctact tattaaaaga aataggcccg 240
 aggcggggcag atcacgaggt caggagatgg agaccactac gtcgatac 288

<210> 197
 <211> 289
 <212> DNA
 <213> Homo sapien

<400> 197
 ttgggcacct tcaatatcat gacagggtgat gtgataacca agaaggctac taagtgatta 60
 atgggtgggt aatgtatata gagtaggtac actggacaga ggggtaattc atagccaagg 120
 caggagaagc agaatggcaa aacatttcat cacactactc aggatagcat gcagtttaaa 180
 acctataagt agtttatttt tggaattttc cacttaatat tttcagactg caggtaacta 240
 aactgtggaa cacaagaaca tagataaggg gagaccacta cgtcgatac 289

<210> 198
 <211> 288
 <212> DNA
 <213> Homo sapien

<400> 198

gtatcgacgt	agtggctctcc	caagcagtgg	gaagaaaacg	tgaaccaatt	aaaatgtatc	60
agatacccca	aagaaaggcg	cttgagtaaa	gattccaagt	gggtcacaa	ctcagatctt	120
aaaattcagg	ctgtcaaaga	gatttgctat	gaggttgctc	tcaatgactt	caggcacagt	180
cggcaggaga	ttgaagccct	ggccattgtc	aagatgaagg	agctttgtgc	catgtatggc	240
aagaaagacc	ccaatgagcg	ggactcctgg	agaccactac	gtcgatac		288

<210> 199

<211> 1027

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1027)

<223> n = A,T,C or G

<400> 199

gctttttggg	aaaaacncaa	ntgggggaaa	gggggnttnn	tngcaagggg	ataaaggggg	60
aancccaggg	tttccccatt	cagggagggtg	taaaaagncg	gccaggggat	tgtaanagga	120
ttcaataata	gggggaatgg	gccnngaagt	tgcaagggtc	cngcccgcca	tgnccgcggg	180
atttagtgac	attacgacgs	tggtataaaa	gtgggsccaa	waaatatttg	tgatgtgatt	240
tttsgaccag	tgaaccatt	gwacaggacc	tcatttctcty	tgagatgrta	gccataatca	300
gataaaaagt	tagaagtytt	tctgcacgtt	aacagcatca	ttaaatggag	tggtcatcacc	360
aattttcacc	tttgtttagcc	gataccttcc	ccttgaaggc	attcaattaa	gtgaccaatc	420
gtcatacgag	aggggatggc	atggggattg	atgatgatat	caggggtgat	accttcacag	480
gtgaaaggca	tatcctcttg	tctatactga	ataccacaag	tacccttttg	accatgtcga	540
ctagcaaatt	tgtctccaat	ctgtgtwac	cctaacagag	cgtaccctta	ttttacaaaa	600
tttatatcct	tcctgattga	gagttaccat	aacctgatcc	acaatgcccg	tctcgctwgt	660
tctgagaaaa	gtgctacagt	ctctcttggt	atagcgtcta	ttggtgctct	ccaattcatc	720
ttcatttttc	aggcaagggtg	aactgttttg	cctataataa	cmtcatctcc	tgatacmcga	780
aacccckgga	rcatatcaaac	catcatcatc	cagcgttckt	watgtymcta	aatccctatt	840
gcggccgcct	gcaggccaac	atatnggaaa	acccccacc	ccttnggagc	ntaccttgaa	900
ttttccatat	gtcccntaaa	ttanctngnc	ttanctggc	cntaacctnt	tccggtttaa	960
attgtttccg	ccccnttcc	ccncccttna	accggaaacc	ttaatttttna	accngggggtt	1020
cctatcc						1027

<210> 200

<211> 207

<212> DNA

<213> Homo sapien

<400> 200

agtgcatta	cgacgctggc	catcttgaat	cctagggcat	gaagttgccc	caaagttcag	60
cacttggtta	agcctgatcc	ctctggttta	tcacaaagaa	taggatggga	taaagaaagt	120
ggacacttaa	ataagctata	aattatatgg	tccttgctta	gcaggagaca	actgcacagg	180
tatactacca	gcgtcgtaat	gtcacta				207

<210> 201

<211> 209

<212> DNA

<213> Homo sapien

<400> 201

tgggcacctt	caatatctat	taaaagcaca	aatactgaag	aacacaccaa	gactatcaat	60
gagggttacat	ctggagtcct	cgatatatca	ggaaaaaatg	aagtgaacat	tcacagagtt	120
ttacttcttt	gggaactcaa	atgctagaaa	agaaaaaggt	gccctcttcc	tctggcttcc	180
tggtcctatc	cagcgtcgta	atgtcacta				209

<210> 202
 <211> 349
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (349)
 <223> n = A,T,C or G

<400> 202						
ntacgctgca	acactgtgga	gccactgggt	tttattcccc	gcaggttatc	cagcaaacag	60
tcactgaaca	caccgaagac	cgtgggtatg	taaccgttca	cagtaatcgt	tccagtcgtc	120
tgcgggaccc	cgacgagcgt	cactgggtac	agaccagatt	cagccggaag	agaaagcgcc	180
gcagggagag	actcgaactc	cactccgctg	gtgagcagcc	ccatgttttc	aactcgaagt	240
tcaaacggca	ttgggttata	taccatcagc	tgaacttcac	acacatctcc	ttgaaccac	300
tggaaatcta	tttctctgtt	ccgctcttct	ccacagtgtt	gcagcgtaa		349

<210> 203
 <211> 241
 <212> DNA
 <213> Homo sapien

<400> 203						
tgctcctctt	gccttaccaa	cccaaagccc	actgtgaaat	atgaagtga	tgacaaaatt	60
cagttttcaa	cgcaatatag	tatagtattat	ctgattcttt	tgatctccag	gacactttta	120
acaactgcta	ccaccaccac	caacctaggg	atttaggatt	ctccacagac	cagaaattat	180
ttctcctttg	agtttcaggc	tcctctggga	ctcctgttca	tcaatgggtg	gtaaattggct	240
a						241

<210> 204
 <211> 248
 <212> DNA
 <213> Homo sapien

<400> 204						
tagccattta	ccaccatct	gcaaaccswg	acmwwcargr	cywgwackya	ggcgatttga	60
agtactggta	atgctctgat	catgttagtt	acataagtgt	ggtcagtta	caaaaattca	120
cagaactaaa	tactcaatgc	tatgtgttca	tgtctgtgtt	tatgtgtgtg	taatgtttca	180
attaagtttt	tttaaaaaaa	agagatgatt	tccaaataag	aaagccgtgt	tggttaaggca	240
agaggagc						248

<210> 205
 <211> 505
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (505)

<223> n = A,T,C or G

<400> 205

tacgtgcaa	cactgtggag	ccattcatac	aggtcacctaa	ttaaggaaca	agtgtattatg	60
ctacctttgc	acgggttaggg	taccgcggcc	gttaaaccatg	tgtcactggg	caggcggtgc	120
ctctaatact	ggatgatgcta	gagggtgatgt	ttttggtaaa	caggcggggt	aagatttgcc	180
gagttccctt	tacttttttt	aacctttcct	tatgagcatg	cctgtgttgg	gttgacagtg	240
ggggaataa	tgacttggtg	gttgattgta	gatattgggc	tgtaattgt	cagttcagt	300
ttttaatctg	acgcaggctt	atgcggagga	gaatgttttc	atgttactta	tactaacatt	360
agttcttcta	taggggtgata	gattgggtcca	attgggtgtg	aggagttcag	ttatatgttt	420
gggatttttt	aggtagtggg	tggtganctt	gaacgccttc	ttaattggtg	gctgctttta	480
rgcctactat	gggtggtaaa	tggt				505

<210> 206

<211> 179

<212> DNA

<213> Homo sapien

<400> 206

tagactgact	catgtcccct	accaaagccc	atgtaaggag	ctgagttcct	aaagactgaa	60
gacagactat	tctctggaga	aaaataaaat	ggaaattgta	ctttaaaaaa	aaaaaaaatc	120
ggcggggcat	ggtagcacac	acctgtaatc	ccagctacta	ggggacatga	gtcagtcta	179

<210> 207

<211> 176

<212> DNA

<213> Homo sapien

<400> 207

agactgactc	atgtccccta	ccccaccttc	tgctgtgtgtg	cctgtgttctt	aacagggtcac	60
agactgggtac	tggtcagtgg	cctggggggt	ggggacctct	attatatggg	atacaaattt	120
aggagttgga	attgacacga	tttagtgact	gatgggatat	gggtggtaaa	tggtcta	176

<210> 208

<211> 196

<212> DNA

<213> Homo sapien

<400> 208

agactgactc	atgtccccta	tttaacaggg	tctctagtgc	tgtgaaaaaa	aaaaatgctg	60
aacattgcat	ataacttata	ttgtaagaaa	tactgtacaa	tgactttatt	gcactctgggt	120
agctgtaagg	catgaaggat	gccaagaagt	ttaaggaata	tggttggtaa	atggctaggg	180
gacatgagtc	agtcta					196

<210> 209

<211> 345

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(345)

<223> n = A,T,C or G

<400> 209

gacgcttggc	cacttgacac	cttttatttt	ttaaggattc	ttaagtcatt	tangtnactt	60
tgtaagtttt	tcctgtgccc	ccataagaat	gatagcttta	aaaattatgc	tggggtagca	120
aagaagatac	ttctagcttt	agaatgtgta	ggtatagcca	ggattcttgt	gaggaggggt	180
gatttagagc	aaatttctta	ttctccttgc	ctcatctgta	acatggggat	aataatagaa	240
ctggcttgac	aagggttgaa	ttagtattac	atggtaaata	catgtaaaat	gtttagaatg	300
gtgccaagta	tctaggaagt	acttgggcat	gggtggtaaa	tggct		345

<210> 210
 <211> 178
 <212> DNA
 <213> Homo sapien

<400> 210						
gacgcttggc	cacttgacac	tagagtaggg	tttggccaac	tttttctata	aaggaccaga	60
gagtaaatac	ttcaggcttt	gtgggttggt	cagtctctct	tgcaactact	cagctctgcc	120
attgtagcat	agaaatcagc	catagacagg	acagaaatga	atgggtggta	aatggcta	178

<210> 211
 <211> 454
 <212> DNA
 <213> Homo sapien

<400> 211						
tgggcacctt	caatatctat	ccagcgcac	taaattcgct	tttttcttga	ttaaaaattt	60
caccacttgc	tgtttttgct	catgtatacc	aagtagcagt	ggtgtgaggg	catgcttggt	120
ttttgattcg	atatcagcac	cgtataagag	cagtgccttg	gccattaatt	tatcttcatt	180
gtagacagca	tagtgtagag	tggtatctcc	atactcatct	ggaatatttg	gatcagtgcc	240
atgttccagc	aacattaacg	cacattcatc	ttcctggcat	tgtacggcct	ttgtcagagc	300
tgctctcttt	ttgttgtaaa	ggacattaag	ttgacatcgt	ctgtccagca	cgagttttac	360
tacttttgaa	ttcccatagg	cagaggccag	atgtagagca	gtcctctttt	gcttgtccct	420
cttgttcaca	tcagtgtccc	tgagcataac	ggaa			454

<210> 212
 <211> 337
 <212> DNA
 <213> Homo sapien

<400> 212						
tccgttatgc	caccagaaa	acctactgga	gttacttatt	aacatcaagg	ctggaacctt	60
tttgccctcag	tcctatctga	ttcatgagca	catgggttatt	actgatcgca	ttgaaaacat	120
tgatcacctg	ggtttcttta	tttatcgact	gtgtcatgac	aaggaaactt	acaaactgca	180
acgcagagaa	actattaaag	gtattcagaa	acgtgaagcc	agcaattggt	tcgcaattcg	240
gcattttgaa	aacaaatttg	ccgtggaaac	tttaatttgt	tcttgaacag	tcaagaaaaa	300
cattattgag	gaaaattaat	atcacagcat	aacggaa			337

<210> 213
 <211> 715
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(715)
 <223> n = A,T,C or G

<400> 213

tcgggtgatg	cctcctcagg	catcttccat	ccatctcttc	aagattagct	gtcccaaagt	60
tttttccttc	tcttctttac	tgataaattt	ggactccttc	ttgacactga	tgacagcttt	120
agtatccttc	ttgtcacctt	gcagacttta	aacataaaaa	tactcattgg	ttttaaaagg	180
aaaaaagtat	acattagcac	tattaagctt	ggccttgaaa	cattttctat	cttttattaa	240
atgtcggtta	gctgaacaga	attcatttta	caatgcagag	tgagaaaaga	agggagctat	300
atgcatttga	gaatgcaagc	attgtcaaatt	aaacatttta	aatgctttct	taaagtgagc	360
acatacagaa	atacattaag	atattagaaa	gtgtttttgc	ttgtgtacta	ctaattaggg	420
aagcaccttg	tatagttcct	cttctaaaat	tgaagtagat	tttaaaaacc	catgtaattt	480
aattgagctc	tcagttcaga	ttttaggaga	attttaacag	ggatttggtt	ttgtctaaat	540
tttgtcaatt	tntttagtta	atctgtataa	ttttataaat	gtcaaactgt	atttagtccg	600
ttttcatgct	gctatgaaag	aaatacccan	gacagggtta	tttataaang	gaaagangtt	660
aatttgactc	ccagttcaca	ggcctgagga	ngnatcnccc	gaaatcctta	ttgcg	715

<210> 214

<211> 345

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (345)

<223> n = A,T,C or G

<400> 214

ggtaangngc	atacntcggg	gctccggccg	ccggagtcgg	gggattcggg	tgatgcctcc	60
tcaggcccac	ttgggcctgc	ttttcccaa	tggcagctcc	tctggacatg	ccattccttc	120
tcccacctgc	ctgattcttc	atatgttggg	tgccctgtt	tttctggtgc	tatttcctga	180
ctgctgttca	gctgccactg	tcctgcaaag	cctgcctttt	taaatgcctc	accattcctt	240
catttgtttc	ttaaataatg	gaagtgaag	tgccacctga	ggccggggcac	agtggctcac	300
gcctgtaatc	ccagcacttt	gggagcctga	ggaggcatca	cccga		345

<210> 215

<211> 429

<212> DNA

<213> Homo sapien

<400> 215

ggtgatgcct	cctcaggcga	agctcaggga	ggacagaaac	ctcccgtgga	gcagaagggc	60
aaaagctcgc	ttgatcttga	ttttcagtac	gaatacagac	cgtgaaagcg	gggcctcacg	120
atccttctga	cctttttggg	tttaagcagg	aggtgtcaga	aaagttacca	cagggataac	180
tggtctgtgg	cggccaagcg	ttcatagcga	cgctgccttt	tgatccttcg	atgtcggctc	240
ttcctatcat	tgtgaagcag	aattcaccaa	gcgttggttt	gttcacccac	taatagggaa	300
cgtgagctgg	gttttagaccg	tcgtgagaca	ggtttagttt	accctactga	tgatgtgtkg	360
ttgccatggt	aatcctgctc	agtacgagag	gaaccgcagg	ttcasacatt	tggtgtatgt	420
gcttgccctt						429

<210> 216

<211> 593

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (593)

<223> n = A,T,C or G

<400> 216
 tgacacctat gtcnngcatc tggtcacagt ttccacaaat agccagcctt tggccacctc 60
 tctgtcctga ggtatacaag tatatcagga ggtgtatacc ttctcttctc ttccccacca 120
 aagagaacat gcaggctctg gaagctgtct taggagcctt tgggctcaga atttcagagt 180
 cttgggtacc ttggatgtgg tctggaagga gaaacattgg ctctggataa ggagtacagc 240
 cggaggaggg tcacagagcc ctacagctcaa gcccctgtgc cttagtctaa aagcagcttt 300
 ggatgaggaa gcagggttaag taacatacgt aagcgtacac aggtagaaaag tgctgggagt 360
 cagaattgca cagtgtgtga gagtagtacc tcaatcaatg agggcaaatac aactgaaaga 420
 agaagaccna ttaatgaatt gcttangggg aaggatcaag gctatcatgg agatctttct 480
 aggaagatta ttgtttanaa ttatgaaagg antagggcag ggacagggcc agaagtanaa 540
 ganaacattg cctatanccc ttgtcttgca cccagatgct ggacaagggtg tca 593

<210> 217
 <211> 335
 <212> DNA
 <213> Homo sapien

<400> 217
 tgacaccttg tccagcatct gacgtgaaga tgagcagctc agaggaggtg tectggattt 60
 cctggttctg tgggctccgt ggcaatgaat tcttctgtga agtggatgaa gactacatcc 120
 aggacaaatt taatcttact ggactcaatg agcaggtccc tcactatcga caagctctag 180
 acatgatctt ggacctggag cctgatgaag aactggaaga caaccccaac cagagtgacc 240
 tgattgagca ggcagccgag atgctttatg gattgatcca cgcccgtctac atccttacca 300
 accgtggcat cgcccagatg ctggacaagg tgtca 335

<210> 218
 <211> 248
 <212> DNA
 <213> Homo sapien

<400> 218
 tacgtactgg tcttgaagggt cttaggtaga gaaaaaatgt gaatatTTta tcaaagacta 60
 tgtatgaaat gggactgttaa gtacagaggg aagggtggcc cttatcgcca gaagtggta 120
 gatgcgtccc cgtcatgaaa tggtgtgtca ctgcccgaca tttgccgaat tactgaaatt 180
 ccgtagaatt agtgcaaatt ctaacgttgt tcatctaaga ttatgggtcc atgtttctag 240
 tactttta 248

<210> 219
 <211> 530
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (530)
 <223> n = A,T,C or G

<400> 219
 tgacgcttgg ccacttgaca caagtagggg ataaggacaa agacccatna ggtggcctgt 60
 cagccttttg ttactgttgc ttccctgtca ccacggcccc ctctgtaggg gtgtgtgtgtg 120
 ctctgtggac attggtgcat ttccacacat accattctct ttctgcttca cagcagtcct 180
 gagggcgggag cacacaggac taccttggtca gatgangata atgatgtctg gccaaactcac 240
 cccccaacct tctcactagt tatangaaga gccangccta naaccttcta tctgncccc 300

ttgccctatg	acctcatccc	tgttccatgc	cctattctga	tttctggtga	actttggagc	360
agcctggttt	ntectectca	ctccagcctc	tctccatacc	atggtanggg	ggtgctgttc	420
cacncaaang	gtcaggtgtg	tctggggaat	cctnananct	gccnggagtt	tcnangcat	480
tcttaaaaac	cttcttgect	aatcanatng	tgtccagtgg	ccaacctn		530

<210> 220

<211> 531

<212> DNA

<213> Homo sapien

<400> 220

tgacgcttgg	ccacttgaca	ctaaatagca	tcttctaaag	gcctgattca	gagttgtgga	60
aaattctccc	agtgtcaggg	attgtcagga	acagggctgc	tcctgtgctc	actttacctg	120
ctgtgtttct	gctggaaaag	gaggggaagag	gaatggctga	tttttaccta	atgtctccca	180
gtttttcata	ttcttcttgg	atcctcttct	ctgacaactg	ttcccttttg	gtcttcttct	240
tcttgctcag	agagcaggtc	tctttaaaaac	tgagaaggga	gaatgagcaa	atgattaaag	300
aaaacacact	tctgaggccc	agagatcaaa	tattaggtaa	atactaaacc	gcttgccctgc	360
tgtggtcact	tttctcctct	ttcacatgct	ctatccctct	atccccacc	tattcatatg	420
gcttttatct	gccaaagttat	ccggcctctc	atcaaccttc	tcccctagcc	tactggggga	480
tatccatctg	ggtctgtctc	tggtgtattg	gtgtcaagtg	gccaaagcgtc	a	531

<210> 221

<211> 530

<212> DNA

<213> Homo sapien

<400> 221

attgacgctt	ggccacttga	cacccgcctg	cctgcaatac	tggggcaagg	gccttcactg	60
ctttcctgcc	accagctgcc	actgcacaca	gagatcagaa	atgctaccaa	ccaagactgt	120
tggtcctcag	cctctctgag	gagaaagagc	agaagcctgg	aagtcagaag	agaagctaga	180
tcggctacgg	ccttggcagc	cagcttcccc	acctgtggca	ataaagtcgt	gcatggctta	240
acaatggggg	cacctcctga	gaaacacatt	gttaggcaat	tcggcggtgtg	ttcatcagag	300
catatttaca	caaacctcga	tagtgacagc	tactatccac	tattgctcct	acgctgcaaa	360
cctgaacagc	atgggactgt	actgaatact	ggaagcagct	ggtgatggta	cttatttgtg	420
tatctaaaca	cagagaaggt	acagtaagaa	tatggtatca	taaacttaca	gggaccgcca	480
tcctatatgc	agtctgttgt	gaccaaaatg	tgtcaagtgy	ccaagcgtca		530

<210> 222

<211> 578

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(578)

<223> n = A,T,C or G

<400> 222

tgtatcgacg	tagtggctct	cgggctacta	ggccgttgtg	tgttggtagt	acctggttca	60
ctgaaaggcg	catctccctc	cccgcgtcgc	cctgaagcag	ggggaggact	tcgccagcc	120
aaggcagttg	tatgagtttt	agctgcggca	cttcgagacc	tctgagccca	cctccttcag	180
gagccttccc	cgattaagga	agccagggtg	aggattcctt	cctccccag	acaccacgaa	240
caaaccacca	ccccccctat	tctggcagcc	catatacatc	agaacgaaac	aaaaataaca	300
aataaacnaa	aaccaaataa	aaaagagaag	gggaaatgta	tatgtctgtc	catcctgttg	360
ctttagcctg	tcagctccta	nagggcaggg	accgtgtcct	ccgaatggtc	tgtgcagcgc	420

cgactgcggg	aagtatcgga	ggaggaagca	gagtcagcag	aagttgaacg	gtgggcccgg	480
cggtctcttg	gggctgggtg	tgtacttcga	gaccgctttc	gctttttgtc	ttagatttac	540
gtttgctctt	tggagtggga	naccactacn	tcnataca			578

<210> 223
 <211> 578
 <212> DNA
 <213> Homo sapien

<400> 223						
tgtatcgacg	tagtgggtctc	ctcttgcaaa	ggactggctg	gtgaatgggt	tccttgaatt	60
atggacttac	cctaaacata	tcttatcatc	attaccagtt	gcaaaatatt	agaatgtggt	120
gtcactgttt	catttgattc	ctagaagggt	agtcttagat	atgttacttt	aacctgtatg	180
ctgtagtgct	ttgaatgcat	tttttgtttg	catttttggt	tgcccaacct	gtcaattata	240
gctgcttagg	tctggactgt	cctggataaa	gctgttaaaa	tattcaccag	tccagccatc	300
ttacaagcta	attaagtcaa	ctaaatgctt	ccttgttttg	ccagacttgt	tatgtcaatc	360
ctcaatttct	gggttcattt	tgggtgccct	aaatcttagg	gtgtgacttt	cttagcatcc	420
tgtaacatcc	attcccaagc	aagcacaaact	tcacataata	ctttccagaa	gttcattgct	480
gaagcctttc	cttcacccag	cggagcaact	tgattttcta	caacttcctc	catcagagcc	540
acaagagtat	gggatatgga	gaccactacg	tcgatata			578

<210> 224
 <211> 345
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (345)
 <223> n = A,T,C or G

<400> 224						
tgtatcgacg	tantgggtctc	ccaagggtgct	gggattgcag	gcatgagcca	ccactcccag	60
gtggatcttt	ttctttatac	ttacttcatt	aggtttctgt	tattcaagaa	gtgtagtggg	120
aaaagtcttt	tcaatctaca	tggttaaata	atgatagcct	gggaaataaa	tagaaatttt	180
ttctttcatc	tttaggttga	ataaagaaac	agaaaaaata	gaacatactg	aaaataatct	240
aagttccaac	catagaagaa	ctgcagaaga	aatgaagaaa	gtgatgatga	tttagatttt	300
gatattgatt	tagaagacac	aggaggagac	cactacgtcg	atata		345

<210> 225
 <211> 347
 <212> DNA
 <213> Homo sapien

<400> 225						
tgtatcgacg	tagtgggtctc	caaactgagg	tatgtgtgcc	actagcacac	aaagccttcc	60
aacagggacg	caggcacagg	cagtttaaag	ggaatctggt	tctaaattaa	ttccacctt	120
ctctaagtat	tctttcctaa	aactgatcaa	gggtgtgaagc	ctgtgctctt	tcccaactcc	180
cctttgacaa	cagccttcaa	ctaacacaag	aaaaggcatg	tctgacactc	ttcctgagtc	240
tgactctgat	acgttggtct	gatgtctaaa	gagctccaga	acaccaaagg	gacaattcag	300
aatgctgggtg	tataacagac	tccaatggag	accactacgt	cgatata		347

<210> 226
 <211> 281
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(281)

<223> n = A,T,C or G

<400> 226

aggngngggga	ntgtatcgac	gtagtgggtct	cccaacagtc	tgtcattcag	tctgcaggtg	60
tcagtgtttt	ggacaatgag	gcaccattgt	cacttattga	ctcctcagct	ctaaatgctg	120
aaattaaatc	ttgtcatgac	aagtctggaa	ttcctgatga	ggttttacaa	agtattttgg	180
atcaatactc	caacaaatca	gaaagccaga	aagaggatcc	tttcaatatt	gcagaaccac	240
gagtggattt	acacacctca	ggagaccact	acgtcgatac	a		281

<210> 227

<211> 3646

<212> DNA

<213> Homo sapien

<400> 227

gggaaacact	tcctccagc	cttgtaagg	ttggagccct	ctccagtata	tgctgcagaa	60
tttttctctc	ggtttctcag	aggattatgg	agtcgcgctt	aaaaaaggca	agctctggac	120
actctgcaaa	gtagaatggc	caaagtttgg	agttgagtgg	ccccctgaag	ggctactgaa	180
cctcacaaat	gttcaagctg	tgtggcgggt	tgttactgaa	actcccggcc	tcctgatca	240
gtttccctac	attgatcaat	ggctgagttt	ggtcaggagc	accccttccg	tggctccact	300
catgcaccat	tcataatttt	acctccaagg	tcctcctgag	ccagaccgtg	ttttcgctc	360
gaccctcagc	cggttcgggt	cgccctgtac	tgcctctctc	tgaagaagag	gagagtctcc	420
ctcaccagct	cccaccgcct	taaaaccagc	ctactccctt	agggtcaccc	catgtctcct	480
cggctatgtc	ccctgtaggc	tcacacacca	ttgcctcttg	ggtgcaaccg	tgggtggagg	540
aagtagcccc	tctactacca	ctgagagagg	cacaagtcct	tctgggtgat	gagtgtccca	600
ccccctcct	ggtttatgtc	ccttctttct	acttctgact	tgtataattg	gaaaaccat	660
aatcctcct	tcctgaaaa	gccccaggct	ttgacctcac	tgatggagtc	tgtactctgg	720
acacattggc	ccacctggga	tgactgtcaa	cagctccttt	tgaccctttt	cacctctgaa	780
gagagggaaa	gtatccaaag	agaggccaaa	aagtacaacc	tcacatcaac	caataggccg	840
gaggaggaag	ctagaggaat	agtgattaga	gacccaattg	ggacctaatt	gggacccaaa	900
tttctcaagt	ggagggagaa	cttttgacga	tttccaccgg	tatctcctcg	tgggtattca	960
gggagctgct	cagaaaccta	taaacttgct	taaggcgact	gaagtcgtcc	aggggcatga	1020
tgagtcacca	ggagtgtttt	tagagcacct	ccaggaggct	tatcagattt	acaccccttt	1080
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ggccctccac	cagcaaaaag	attctgactc	actgaagact	tggatgatca	ttagtatttt	3600
tagcagtaaa	gttttttttt	ctttttcttt	ctttttttct	cgtgcc		3646

<210> 228

<211> 419

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(419)

<223> n = A,T,C or G

<400> 228

taagagggtta	caagatctaa	gcacagccgt	caatgcagaa	cacagaacgt	agcctggtaa	60
gtgtgttaag	agtgggaatt	tttggagtac	agagtaaggc	acctaaccct	agctgggggtt	120
tggtgacggg	cccagatggc	ttacagaaga	aagtgtcctg	agatgagttt	ttaagaatga	180
ataaggatag	acacaagtga	ggactgactt	ggcagtgggtg	aatgggtgggt	ggcaaaaaac	240
ttcgcatgta	tggaaaactgc	acgtacagga	atgaagaatg	agactgtgtg	gtgtttaatg	300
agctgcaaat	actaatttta	tcctgaaagt	tttgaagagt	taactaaaaa	gtatttttta	360
gtaaggaaat	aaccctacat	ttcagggtta	ttgtttgttt	anatattgaa	ggtgcccaa	419

<210> 229

<211> 148

<212> DNA

<213> Homo sapien

<400> 229

aagagggtac	ctgtatgtag	ccatgggtggc	aatgagagac	tgattactac	ctgctggaga	60
ttgtttaagt	gagttaatat	attaaggata	aaggagacca	ggttttttga	ctgttgagga	120
aggaaattac	agatattgaa	ggtcccaa				148

<210> 230
 <211> 257
 <212> DNA
 <213> Homo sapien

<400> 230
 taagaggggta cmaaaaaaaaaaaa aaaatagaac gaatgagtaa gacctactat ttgatagtagt 60
 aacaggggtga ctatagtcac tgataactta attatacatt taacatagag tgtaattgga 120
 ttgtttgttaa ctggaaggat aaatgcttga gaggatggat accccattct ccatgatgta 180
 cttatttcac attacatgcc tgtatcaaag catctcatat accctataaa tatgtacacc 240
 tactatgtac cctctta 257

<210> 231
 <211> 260
 <212> DNA
 <213> Homo sapien

<400> 231
 taagaggggta cgggtatttg ctgatgggat ttttttttct ttctttttct ttggaaaaca 60
 aaatgaaagc cagaacaaaa ttattgaaca aaagacaggg actaaatctg gagaaatgaa 120
 gtccctcac ctgactgcca ttctattcta tctgaccttc cagtctaggt taggagaata 180
 gggggtggag gggattaatc tgatacaggt atatttaaag caactctgca tgtgtgccag 240
 aagtccatgg taccctctta 260

<210> 232
 <211> 596
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (596)
 <223> n = A,T,C or G

<400> 232
 tgctcctctt gccttaccaa ccacaaatta gaaccataat gagatgtcac ctcatacctg 60
 gtgggattaa cattatttaa aaaatcagaa gtattgacaa ggatgtgaag aaattagaac 120
 atctgtgcac tggttggtgg aatgtaaaaa aggtgtggcc actatgggta acagcatgaa 180
 ggttcctcaa aaaaaatttt ttttaattcta ctctatgatc gatcttgagg ttgtttatgc 240
 aaaagaactg aaatcaggat tttgaggaaa tattcacatt cccacatcca tttctgcttt 300
 attcataata ctcaagagat ggaaacaacc taaatgtcca tcccgggatg aatggataaa 360
 cacagtgtgg tatatgcata caatggaata ttatttagtc tttaaaaaga aaaattctat 420
 catatactac aacttanatn aaccttgagg acacaatgct nagtgaaata agccacggaa 480
 ggacgaatac tgcattatc ccttatatga agtatctaaa gtggtcaaac tcttanagca 540
 naaagtaaaa atgggtgggt gccanacagt tgggttaggcn agaaganaan cctant 596

<210> 233
 <211> 96
 <212> DNA
 <213> Homo sapien

<400> 233
 tcttctgaag acctttcgcg actcttaagc tctgtggttg taaggcaaga ggagcgttgg 60
 taaggcaaga ggagcgttgg taaggcaaga ggagca 96

<210> 234
 <211> 313
 <212> DNA
 <213> Homo sapien

<400> 234
 tgtaagtcca gcagtgtgat gataaaactt gaatggatca atagttgctt cttatggatg 60
 agcaaagaaa gtagtttctt gtgatggaat ctgtccttg caaaaatgct gtgaacgttg 120
 ttgaaaagac aacaaagagt ttagagtagt acataaattt agaatagtag ataaacttag 180
 aatagtagat aaacttagta cataaataat gcacgaagca ggggcagggc ttgagagaat 240
 tgacttcaat ttggaaagag tatctactgt aggttagatg ctctcaaaca gcatcacact 300
 gctcgactta caa 313

<210> 235
 <211> 550
 <212> DNA
 <213> Homo sapien

<400> 235
 aacgaggaca gaccccttaa aagaatgttg agtgaaaaaa gtagaaaata agataatctc 60
 caaagtccag tagcattatt taaacatttt taaaaaatac actgataaaa attttgtaca 120
 tttcccaaaa atacatatgg aagcacagca gcatgaatgc ctatgggrtt gaggataggg 180
 gttggggagta gggatgggga taaaggggga aaataaaacc agagaggagt cttacacatt 240
 tcatgaacca aggagtataa ttatttcaac tatttgtacc wgaagtccag aaagagtggga 300
 ggcagaaggg ggagaagagg gcgaagaaac gtttttggga gaggggtccc asaagagaga 360
 ttttcgcgat gtggcgctac atacgttttt ccaggatgcc ttaagctctg caccctatct 420
 ttctcatcac taatattaga ttaaaccctt tgaagacagc gtctgtgggt tctctacttc 480
 agctttccct ccgtgtcttg cacacagtag ctgttttaca aggggtgaac tgactgaagt 540
 gagattatct 550

<210> 236
 <211> 325
 <212> DNA
 <213> Homo sapien

<400> 236
 tagactgact catgtccctt accagagtag ctagaattaa tagcacaagc ctctacaccc 60
 aggaactcac tattgaatac ataaatggaa tttattcagc cttaaaaagt ttggaaggaa 120
 attctgacat atgctaaaac atggatgaac cttgaagact ttatgataag taaaagaagc 180
 cagtcataaa aggaaaaata ttgcatgatt ccacttatat gaggtaccta gagtagtcaa 240
 tttcatagaa acacaaaata gaatggtgtt tgccagggct tttgaggaaa aggggaatgac 300
 aagttagggg acatgagtca gtcta 325

<210> 237
 <211> 373
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (373)
 <223> n = A,T,C or G

<400> 237

```

tagactgact catgtcccct atctactcaa catttccact tgaagtctga taggcatctc      60
agacttatct tgteccaaag caaactcttt atttcttttc atcctagtct ttatttcttg      120
tgctgtctta cccatctcaa aagagtgcc aatccacca agttgctgaa acagaaatct      180
aagaaatatt cttgattctt ctttttccca tctacttcac ttctaattca ttagtaaata      240
atctgtttca gaaaaccaa cacctcatgt tctcactcat aagggggagt tgaacaatga      300
gaacacacag acacagggag gggaacatca cacaccacgg ccggtcaggg agtangggac      360
atgagtcagt cta                                     373

```

```

<210> 238
<211> 492
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(492)
<223> n = A,T,C or G

```

```

<400> 238
tagactgact catgtcccct ataatgtctc caggcatcag aaagcatctc aaactggagc      60
tgacaccatg gcagagggtt caggtaagtc acaaaagggg tcctaaagaa ttgcccctca      120
atatcagagt gattagaaga agtggacaga gctacccaag ttaaaccatat gcgagataaa      180
aaaaatatgg cacttgtgaa cacacactac aggaggaaaa taaggaaacat aatagcatat      240
tgtgtctatta tgatgatgaa gaacctctct anaagaaaac ataaccaaag aaacaaagaa      300
aattcctgcn aatgtttaat gctatagaag aaattaacaa aaacatatat tcaatgaatt      360
cagaaaagtt agcaggtcan aagaaaacaa atcaaagacc agaataatcc catttttagat      420
tgtcgagtaa actanaacag aaagaatacc actggaaatt gaattcctac gtangggaca      480
tgantcanc ta                                     492

```

```

<210> 239
<211> 482
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(482)
<223> n = A,T,C or G

```

```

<400> 239
tggaaagtat ttaatgatgg gcaacttgct gtttacttcc tacatatccc atcatcttct      60
gtattttttt aaataacttt tttttggatt tttaaagtaa ctttattctg agaggtaaca      120
tggattacat acttctaagc cattaggaga ctctatgtta aaccaaagg aaatgttact      180
agatcttcat ttgatcaata ggatgtgata atcatcatct ttctgctcta atggaaaagt      240
actanaaaaca tggaaccata atcttagatg aacaacgtta gaatttgcac taattctacg      300
gaatttcagt aattcggcaa atgtcgggca gtgacacaac atttcatgac ggggacgcat      360
ctaccaactt ctggcgataa gggccacct tccctctgta cttacagtcc catttcatac      420
acagtctttg attaaatatt cacatttttt ctctacctaa agaccttcaa gaccagtacg      480
ta                                     482

```

```

<210> 240
<211> 519
<212> DNA
<213> Homo sapien

```

<220>
 <221> misc_feature
 <222> (1)...(519)
 <223> n = A,T,C or G

<400> 240
 tgtatcgacg tagtggtctc cccatgtgat agtctgaaat atagcctcat gggatgagag 60
 gctgtgcccc agcccgacac ccgtaaaggg tctgtgctga ggtggattag taaaagagga 120
 aagccttgca gttgagatag aggaagggca ctgtctcctg cctgccccctg ggaactgaat 180
 gtctcggtat aaaacccgat tgtacatttg ttcaattctg agataggaga aaaaccaccc 240
 tatggcggga ggcgagacat gttggcagca atgctgcctt gttatgcttt actccacaga 300
 tgtttgggcg gagggaaaca taaatctggc ctacgtgcac atccaggcat agtacctccc 360
 tttgaactta attatgacac agattccttt gctcacatgt ttttttgctg accttctcct 420
 tattatcacc ctgctctcct accgcattcc ttgtgctgag ataatgaaaa taatatcaat 480
 aaaaacttga nggaactcgg agaccactac gtcgatata 519

<210> 241
 <211> 771
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(771)
 <223> n = A,T,C or G

<400> 241
 tgtatcgacg tagtggtctc cactccccgcc ttgacggggc tgctatctgc cttccaggcc 60
 actgtcacgg ctccccggta gaagtcactt atgagacaca ccagtgtggc cttgttggct 120
 tgaagctcct cagaggaggg tgggaacaga gtgaccgagg gggcagcctt gggctgacct 180
 aggacggta gcttggtccc tccgccaaac acgagagtgc tgctgcttgt atatgagctg 240
 cagtaataat cagcctcgtc ctcagcctgg agcccagaga tggtcaggga ggccgtgttg 300
 ccanacttgg agccagagaa gcgattagaa acccctgagg gccgattacc gacctcataa 360
 atcatgaatt tgggggcttt gctgggtgc tgttggtacc angagacatt attataacca 420
 ccaacgtcac tgetggttcc antgcaggga aaatggttga tcnaactgtc caagaaaacc 480
 actacgtcca taccaatcca ctaattgccn gccgcctgca ggttcaacca tattggggaa 540
 naactcccn cgcgcgtttg ggattgncat naacctttga aattttttcc tattanttgt 600
 cccctaaaa taaacnttg ggcnttaatc cattgggtcc atancttntt tncccggttt 660
 ttaaaanttg tttatcccgc cncctnattt ccccccaac tttccaaaac ccgaaacctt 720
 tnaaatttnt tnaaacctg gggggttccc nnaattnnan ttnaanctnc c 771

<210> 242
 <211> 167
 <212> DNA
 <213> Homo sapien

<400> 242
 tgggcacctt caatatcgga ctcatcgata acatcacgct gctgatgctg ctggtgctgg 60
 tctctcttag gaacctctgg attttcaaat tctttgagga attcatccaa attatctgcc 120
 tctctcctt tctctctttt tctaaggctc tctgggtacaa gcgggtca 167

<210> 243
 <211> 338
 <212> DNA
 <213> Homo sapien

<400> 243

ttgggcacct	tcaatatcta	ctgatctaaa	tagtgtgggt	tgaggcctct	tgttctctggc	60
taaaaatcct	tggcaagagt	caatctccac	tttacaatag	aggtaaaaat	cttacaatgg	120
atattcttga	caaagctagc	atagagacag	caattttaca	caagggtattt	ttcacctggt	180
taataacagt	ggtttttcta	cacccatagg	gtgccaccaa	gggaggagtg	cacagttgca	240
gaaacaaatt	aagatactga	agacaacact	acttaccatt	tcccgtatag	ctaaccacca	300
gttcaactgt	acatgtatgt	tcttatgggc	aatcaaga			338

<210> 244

<211> 346

<212> DNA

<213> Homo sapien

<400> 244

tttttggttc	ccatacagca	cactctcatg	ggaaatgtct	gttctaaggt	caaccataa	60
tgcaaaaatc	atcaatatac	ttgaagatcc	ccgtgtaagg	tacaatgtat	ttaatatatt	120
cactgataca	attgatccaa	taccagtttt	agtctggcat	tgaatcaa	cactgttttt	180
gttgataaaa	aagagaaata	tttagcttat	atttaagtac	catattgtaa	gaaaaaagat	240
gcttatcttt	acatgctaaa	atcatgatct	gtacattggt	gcagtgaata	ttactgtaaa	300
agggagaag	gaatgaagac	gagctaagga	tattgaaggt	gcccaa		346

<210> 245

<211> 521

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(521)

<223> n = A,T,C or G

<400> 245

accaatccca	cacggatact	gagggacaag	tatatcatcc	catttcatcc	ctacagcagc	60
aacttcatga	ggcaggaggt	attagtccca	ttttacagaa	gaggaaactg	agacttaggg	120
agatcaagta	atttgcccag	gtgcacaa	tagtgataga	gccagggtct	gaagcgacgt	180
ctgtcttaag	ccaatgaccc	ctgcagatta	ttagagcaac	tgttctccac	aacagtgtaa	240
gcctcttget	anaagctcag	gtccacaagg	gcagagattt	ttgtctgttt	tgctcattgc	300
tccttcccca	ttgcttagag	cagggctctgc	cacgaancag	gttctcaatg	catagttatt	360
aaatgtatat	aagagcaaac	atatgttaca	gagaactttc	tgtatgcttg	tcacttacat	420
gaatcacctg	tganatgggt	atgcttggtc	cccantgttg	cagatnaaga	tattgaangt	480
gcccaaatca	ctanttgcg	gcgcctgcan	gtccancata	t		521

<210> 246

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(482)

<223> n = A,T,C or G

<400> 246

tggaaccaat	ccaaataccc	atcaatgata	gactggataa	agaaaatttg	gcacatgttc	60
------------	------------	------------	------------	------------	------------	----


```

accatgaaat actatgcagc cataaaaaag gatgagttca tatectttgc agggacatgg      120
atgaagctgg agaccatcat tctcagcaaa ctaacaaggg aacagaaaac caaacactgc      180
atgtttctcac tcttaagtgg gagctgaaca atgagaacac atggacacag ggaggggaac      240
atcacacagt ggggcctgct ggtgggtagg ggtctagggg agggatagca ttaggagaaa      300
tacctaattg agatgacggg ttgatgggtg cagcaaacca ccatgacacg tgtataccta      360
tgtaacaaac ctgcatgttc tgcacatgta cccagaact taaagtgtta ataaaaaat      420
taagaaaaaa gttaagtatg tcatagatac ataaaatatt gtanatattg aagggtgccca      480
aa

```

<210> 247

<211> 474

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (474)

<223> n = A,T,C or G

<400> 247

```

ttcgatacag gcacagagta agcagaaaaa tggctgtggt ttaaccaagt gagtacagtt      60
aagtgaagaga ggggcagaga agacaagggc atatgcaggg ggtgattata acaggtgggt      120
gtgctgggaa gtgaggggtac tcggggatga ggaacagtga aaaagtggca aaaagtggta      180
agatcagtga attgtacttc tccagaattt gatttctggn ggagtcaaat aactatccag      240
tttgggggtat catanggcaa cagttgaggt ataggaggta gaagtencag tgggataatt      300
gaggttatga anggtttggt actgactggt actgacaang tctgggttat gaccatggga      360
atgaatgact gtanaagcgt anaggatgaa actattccac ganaaagggg tccnaaaact      420
aaaaannnaa gnnnnnnggg aatattattt atgtggatat tgaangtgcc caaa      474

```

<210> 248

<211> 355

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (355)

<223> n = A,T,C or G

<400> 248

```

ttcgatacag gcaaacatga actgcaggag ggtggtgacg atcatgatgt tgccgatgggt      60
ccggatggnc acgaagacgc actggancac gtgcttacgt ccttttgctc tgttgatggc      120
cctgagggga cgcaggaccc ttatgacctt cagaatcttc acaacgggag atggcactgg      180
attgantccc antgacacca gagacacccc aaccaccagn atatcantat attgatgtag      240
ttcctgtaga nggccccctt gtggaggaaa gctccatnag ttggtcatct tcaacaggat      300
ctcaacagtt tccgatggct gtgatgggca tagtcatant taacentgtn tcgaa      355

```

<210> 249

<211> 434

<212> DNA

<213> Homo sapien

<400> 249

```

ttggattggt cctccaggag aacaagggga aaaaggtgac cgaggggtcc ctggaactca      60
aggatctcca ggagcaaaaag gggatggggg aattcctggt cctgctggtc ccttaggtcc      120

```

acctggctcct	ccaggccttac	caggtcctca	aggcccaaag	ggtaacaaag	gctctactgg	180
acccgctggc	cagaaagggtg	acagtgggtct	tccagggcct	cctggggcctc	caggtccacc	240
tgggtgaagtc	attcagcctt	taccaatctt	gtcctccaaa	aaaacgagaa	gacatactga	300
aggcatgcaa	gcagatgcag	atgataatat	tcttgattac	tcggatggaa	tggaagaaat	360
atttggttcc	ctcaattccc	tgaacaaga	catcgagcat	atgaaatttc	caatgggtac	420
tcagaccaat	ccaa					434

<210> 250

<211> 430

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(430)

<223> n = A,T,C or G

<400> 250

tggattgggtc	acatggcaga	gacaggattc	caaggcagtg	agaggaggat	acaatgcttc	60
tcactagtta	ttattattta	ttttattttt	gagatgaagt	ctcgctttgt	ctcccaggct	120
ggagagcggt	ggtgcgatct	tggctctctg	caacccccgc	ctcaagcaat	tctcctgtct	180
tagcctcgcg	ggtagatgga	attacaggcg	cccaccgcca	tgcccaacta	atTTTTTTgt	240
gtcttcagta	gagacagggt	ttcgccatgt	tgggcaggct	ggtcttgaac	tcctgacctc	300
nagtgatctg	ccctcctcgg	cctcacaag	tgctggaatt	acaggcatgg	gctgctgcac	360
ccagtcaact	tctcactagt	tatggcctta	tcattttcac	cacattctat	tggcccaaaa	420
aaaaaaaaan						430

<210> 251

<211> 329

<212> DNA

<213> Homo sapien

<400> 251

tggactacca	ccatyatggg	gtcaaccgcc	atcctcgccc	tctcctggc	tgttctccaa	60
ggagtctgtg	ccgaggtgca	gctgrtgag	tctggagcag	aggtgaaaaa	gtccggggag	120
tctctgaaga	tctcctgtaa	gggttctgga	tacaccttta	agatctactg	gatcgcttgg	180
gtgcgccagt	tgcccgggaa	aggcctggag	tggatggggc	tcattctttc	tgatgactct	240
gataccagat	acagcccgtc	cttccaaggc	cagggtcacca	tctcagtcga	taagtccatc	300
agcaccgcct	atctgcagtg	gagtaccaa				329

<210> 252

<211> 536

<212> DNA

<213> Homo sapien

<400> 252

tggactacca	ctcagcccaa	ccttaattaa	gaattaagag	ggaacctatt	actattctcc	60
caggctcctc	tgctctaacc	aggcttctgg	gacagtatta	gaaaaggatg	tctcaacaag	120
tatgtagatc	ctgtactggc	ctaagaagtt	aaactgagaa	tagcataaat	cagaccaaac	180
ttaatggtcg	ttgagacttg	tgtcctggag	cagctgggat	aggaaaactt	ttgggcagca	240
agaggaagaa	ctgcctggaa	gggggcatca	tgttaaaaat	tacaagggga	acccacacca	300
ggcccccttc	ccagctctca	gcctagagta	ttagcatttc	tcagctagag	actcacaact	360
tccttgctta	gaatgtgcc	ccggggggag	tcctgtggg	tgatgaggct	ctcaagagtg	420
agagtggcat	cctatcttct	gtgtgccac	aggagcctgg	cccagactt	agcaggtgaa	480
gtttctggtc	caggctttgc	ccttgactca	ctatgtgacc	tctggtggag	taccaa	536

<210> 253
 <211> 507
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(507)
 <223> n = A,T,C or G

<400> 253
 ntgttgccgat cccagtaact cgggaagctg aggcggggagg atcacctgag ctcaggagggt 60
 tgaggccgca gtgagccggg accacgccac tacactccag cctggggcat agagtgagac 120
 cctccaagac agaaaaagaaa agaaaggaag ggaaagggaa agggaaaagg aaaaggaaaa 180
 ggaaaaggaa aaggaaaaga caagacaaaa caagacttga atttggtatct cctgacttca 240
 attttatgtt ctttctacac cacaattcct ctgcttacta agatgataat ttagaaaccc 300
 ctggttccat tctttacagc aagctggaag tttggtcaag taattacaat aatagtaaca 360
 aatttgaata ttatatgccg ggtgtttttc attcctgctc tcacttaatt ctcaccactc 420
 tgatataaat acaattgctg ccgggtgtgg tggctcatgc ctgtaatccc ggcacttttg 480
 gagaccgagg tgggcggtats gcaacaa 507

<210> 254
 <211> 222
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(222)
 <223> n = A,T,C or G

<400> 254
 ttggattggt cactgtgagg aagccaaatc ggatccgaga gtctttttct aaaggccagt 60
 actggccaca ctttctcctg ccgccttccct caaagctgaa gacacacaga gcaaggcgct 120
 tctgttttac tccccaatgg taactccaaa ccatagatgg ttagctnccc tgctcatctt 180
 tccacatccc tgctattcag tatagtcctg ggaccaatcc aa 222

<210> 255
 <211> 463
 <212> DNA
 <213> Homo sapien

<400> 255
 tgttgccgac cataaatgct gaaatggaaa taaacaacat gatgagggag gattaagttg 60
 gggaggggagc acattaaggt ggccatgaag tttgttgga gaagtgactt ttgaacaagg 120
 ccttggtggt aagagctgat gagagtgtcc cagacagagg ggccactggt acaatagacg 180
 agatgggaga gggcttgga ggtgtgcaaa ataggaagga gtttgttctg gtatgagtct 240
 agtgaacaca gaggcgagag gccctggtgg gtgcagctgg agagttatgc agaataacat 300
 taggcctgt gggggactgt agactgtcag caataatcca cagtttggat tttattctaa 360
 gagtgatggg aagccgtgga aaggggggta agcaaggagt gaaattatca gatttacagt 420
 gataaaaaata aattggtctg gctactgggg aaaaaaaaaa aaa 463

<210> 256
 <211> 262

<212> DNA
<213> Homo sapien

<400> 256
 ttggattggg caacctgctc aactctacyt ttctctcttc ttctctaaaa attaatgaat 60
 ccaatacatt aatgccaaaa ccttgggggt ttatcaatat ttctgttaaa aagtattatc 120
 cagaactgga cataatacta cataataata cataacaacc ccttcatctg gatgcaaaca 180
 tctattaata tagcttaaga tcactttcac ttacagaag caacatcctg ttgatgttat 240
 tttgatgttt ggaccaatcc aa 262

<210> 257
 <211> 461
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(461)
 <223> n = A,T,C or G

<400> 257
 gnggnnnnnn nnncaattcg actcngttcc cntgggtancc ggctcgacatg gccgcgggat 60
 taccgcttgt nntcgggggt gtatggggga ctatgaccgc ttgtagctgg ggggtgatgg 120
 gggactatga ccgcttgtag mtggkgggtg atgggggact atgaccgctt gtcgggtggg 180
 cggataaacc gacgcaaggg acgtgatcga agctgcgttc ccgctcttcc gcatcggtag 240
 ggatcatgga cagcaatata cgcattcgyt tgaaggcggt cgaccatcgc gtgctcgatc 300
 aggcgaccgg cgacatcgcc gacaccgcac gccgtaccgg ccgctcatc ccgggtccga 360
 tcccgttcc caccgcatc gagaagttca cgggtcaaccg tggcccgcac gtcgacaaga 420
 agtcgcgcga gcagttcgag gtgcgtacct acaagcggtc a 461

<210> 258
 <211> 332
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(332)
 <223> n = A,T,C or G

<400> 258
 tgaccgcttg tagctggggg tgtatggggg actacgaccg cttgtagctg ggggtgatg 60
 ggggactatg accgcttgta gctgggggtg tatgggggac tatgaccgct tgtagctggg 120
 ggtgatggg ggactaggac cgcttgtagc tgggggtgta tgggggacta tgaccgcttg 180
 tagctggggg tgtatggggg actacgaccg cttgtagctg ggggtgatg ggggactatg 240
 accgcttgta nctgggggtg tatgggggac tatgaccgct tgtgctgcct gggggatggg 300
 aggagagttg tggttgggga aaaaaaaaaa aa 332

<210> 259
 <211> 291
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1) ... (291)

<223> n = A,T,C or G

<400> 259

taccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt	60
gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt	120
gaccgcttgt gaccgcttgt nacnggggggt gtctggggga ctatgannga ntgtnactgg	180
gggtgtcttg gggncatga nngantgtna cnggggggtgt ctgggggact atganngact	240
gtgcnnctg ggggatcnga ggagantngn ggntagngat ggttngggan a	291

<210> 260

<211> 238

<212> DNA

<213> Homo sapien

<400> 260

taagagggtta ctgggttaaaa tacaggaaat ctggggtaat gaggcagaga accaggatac	60
tttgagggtca gggatgaaaa ctagaatttt tttctttttt ttgcctgag aaacttgctg	120
ctctgaagag gcccatgtat taattgcttt gatcttcctt ttcttacagc cttttcaagg	180
gcagagccct cttatcctg aaggaatctt atccttagct atagtatgta ccctctta	238

<210> 261

<211> 746

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (746)

<223> n = A,T,C or G

<400> 261

ttgggcacct tcaatatcaa tagctaacat ttattgagtg tttatcgat cataaaacac	60
tggttctaagc ctttaaacgt actaattcat ttaatgctca taatcacttt agaagggtggg	120
tactagtatt agtctcattt acagatgcaa catgcaggca cagagagggt aattaacttg	180
cccaaggtaa cacagctaag aaatagaaaa aatattgaat ctggaaagtt gggcttcttg	240
gtaaccacaca gagtcttcaa tgagcctggg gcctcactca gtttgctttt acaaagcgaa	300
tgagtaacat cacttaattc agtgagtagg ccaaatggag gtcagctacg agtttctgct	360
gttcttgtag tggactgaca gatgtttaca acgtctggcc atcagtwaat ggactgatta	420
tcattgggaw gtgggtgggc tgaatgttgg ccagtgaagt ttattcawgc catattttta	480
tgtttaggat gacttttggc tggctcctagg gcaagctctg tctgscacgg aacacagaat	540
wacacagga cccctcaat ttctggtgtg gctagaacca tgaaccactg gttgggggaa	600
caagcgggtca aaacctaat gcggccggct ggcagggtcc acccatatgg ggaaaactcc	660
cnacgcgttt ggaatgcctn agctngaatt attctaana ttgtccnct aaaattagcc	720
tgggcggtta tcangggctn naagc	746

<210> 262

<211> 588

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (588)

<223> n = A,T,C or G

<400> 262

tgaccgcttg	tcattctcaca	tgggggtcctg	cacgcttttg	cctttgtagg	aaacctgaca	60
tttgtctgtt	tettctttct	cttttctctc	ccatatactc	ctaatttacg	tttgacttgt	120
ttgctgagga	ggcaggagct	agagactgct	gtgagctcat	aggggtggga	agtttatcct	180
tcaagtcccg	cccactcatc	actgcttctc	accttccctc	gaccaggctt	acaagtgggt	240
tcttgctgc	tttccctttg	gacccaacaa	gccctgttaa	tgagtgtgca	tgactctgac	300
agctgtggac	tcagggtcct	tggctacagc	tgccatgtaa	aatatctcat	ccagttctcg	360
caaattgtta	aaataaccac	atttcttaga	ttccagtacc	caaatcatgt	ctttacgaac	420
tgctcctcac	acccagaagt	ggcacaataa	ttcttgggga	attattactt	ttttttttct	480
ctctnttnnc	gnnnngnnng	gnnnngnccag	gaattaccac	nttggaagac	ctggccngaa	540
tttattatan	agggggagccg	attntttttc	ctaacacaaa	gcgggtca		588

<210> 263

<211> 730

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(730)

<223> n = A,T,C or G

<400> 263

tttttttttt	tttggcctga	gcaactgaaa	ttatgaaatt	tccatatact	caaaagagta	60
agactgcaaa	aagattaaat	gtaaaagttg	tcttggtatac	agtaatgttt	aagataccta	120
ttanatttat	aaatggaaaa	ttagggcatt	tggtatataca	agttgaaaat	tcaggagtga	180
ggttgggctg	gctgggtata	tactgaaaac	tgtcagtaca	cagatgacat	ctaaaaccac	240
aaatctgggt	ttatttttagc	agtgatatgt	gtcactccca	caaaagcctt	cccaattggc	300
ctcagcatat	acaacaagtc	acctccccac	agccctctac	acataaacia	attccttagt	360
ttagttcagg	aggaaatgcg	cccttttctc	tccgctctag	gtgaccgcaa	ggcccagttc	420
tcgtcaccaa	gatgttaagg	gaagtctgcc	aaagaggcat	ctgaaaggaa	ataaggggaa	480
tgggagtgc	cacaaaaggaa	agccaaggan	aaactttgga	gaccgtttct	aganccttgg	540
catttcacaa	caaaactcng	gaacaaacct	tgtctcatca	atcatttaag	cccttcgttt	600
ggannagact	ttctgaactg	ggcgtgaac	ataancctca	ttgaatgtct	tcacagtctc	660
ccagctgaag	gcacaccttg	ggccagaagg	ggaatcttcc	aggtcctcaa	nacagggtctc	720
gccctttgnc						730

<210> 264

<211> 715

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(715)

<223> n = A,T,C or G

<400> 264

tttttttttt	tttggccagt	atgatagtct	ctaccactat	attgaagctc	ttaggtcatt	60
tacacttaat	gtgggttatag	atgctgttga	gcttacttct	accaccttgc	tatttctccc	120
gtctcttttt	tgttcttttt	ctcttctttt	cctcccttat	tttataattg	aatttttttag	180
gattctattt	tatatagatt	tatcagctat	aacactttgt	attctttttgt	tttgtgggtc	240
ttctgtcatt	tcaatgtgca	tcttaaaactc	atcacaatct	attttcaaata	aatatcatat	300
aaccttacat	ataatgtaag	aatctaccac	catatatttc	catttctccc	ttccatccta	360

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tgtntgtcat attttttctt ttatatatgt tttaaagaca taatagtata tgggaggttt      420
ttgcttaaaa tgtgatcaat attccttcaa ngaaacgtaa aaattcaaaa taaatntctg      480
tttattctca aatnnaccta atatttecta ccatntctna tacntttcaa gaatctgaag      540
gcattgggtt tttccggctt aagaacctcc tctaaagcac tctaagcaga attaagtctt      600
ctgggagagg aattctccca agcttgggccc ttnanntgta ctcctnang gttaaanttt      660
ggccgggaaa tagaaattcc aagttaacag gntanttttt nttttnttn tcncc          715

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<210> 265
<211> 152
<212> DNA
<213> Homo sapien

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<400> 265
tttttttttt tttcccaaca caaagcacca ttatctttcc tcacaatttt caacatagtt      60
tgattcccat gaagagggtta tgatttctaa agaaaacatg gctactatac tatcaatcag      120
ggttaaatct tttttttttg agacggagtt ta                                152

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<210> 266
<211> 193
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(193)
<223> n = A,T,C or G

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<400> 266
taaactccgt ccccttctta atcaatatgg aggctaccca ctccacatta ccttcttttc      60
aagggactgt ttccgtaact gttgtgggta ttcacgacca ggcttctaaa cctcttaaaa      120
ctccccaatt ctggtgccaa cttggacaac atgctttttt tttttttttt ttttttttn      180
gagacggagt tta                                193

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<210> 267
<211> 460
<212> DNA
<213> Homo sapien

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<400> 267
tgttgcgatc cettaagcat ggggtgtatt aaaaaaatgg tggagaagaa aatacctgga      60
atttacgtct tatctttaga gattgggaag accctgatgg aggacgtgga gaacagcttc      120
ttcttgaatg tcaattccca agtaacaaca gtgtgtcagg cacttgctaa ggatcctaaa      180
ttgcagcaag gctacaatgc tatgggattc tcccaggagg gccaatctct gagggcagtg      240
gctcagagat gcccttcacc tcccatgac aatctgatct cggttggggg acaacatcaa      300
gggtgttttg gactccctcg atgccagga gagagctctc acatctgtga cttcatccga      360
aaaacactga atgctggggc gtactccaaa gttgttcagg aacgcctcgt gcaagccgaa      420
tactggcatg acccataaaa ggaggatgtg gatcgcaaca                                460

```

```

<210> 268
<211> 533
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature

```

<222> (1)...(533)

<223> n = A,T,C or G

<400> 268

tggttgcgac	cgttgataga	atagcgacgt	ggtaatgagt	gcatygcacg	cctccgactt	60
accttgcgcc	gtggggaccc	cgagtacgtc	tacggcgctc	tcacttagag	taccctctgg	120
acgcccgggc	gcgttcgatt	taccggaagc	gcgagctgca	gtgggcttgc	gcccccggcc	180
aaattctttg	gggggtttta	ggccgcgggg	aatttgaggt	atctctatca	gtatgtagcc	240
aagttggaac	agtcgccatt	cccgaatcg	ctttctttga	atccgcaccg	cctccagcat	300
tgcttcattc	atcaacctga	aggcacgcat	aagtgcgggt	tgtgtcttca	gcagctccac	360
tccataacta	gcgcgctcga	cctcgtcttc	gtacgcgcca	ggcccgctgc	tgcgaaattcc	420
caactccggt	gagttgcgca	tttcaagttt	cgaaactgtt	cgctccacn	atttggcatg	480
ttcacgcatg	acacggaata	aactcgtcca	gtaccgggaa	tgggategca	aca	533

<210> 269

<211> 50

<212> DNA

<213> Homo sapien

<400> 269

tttttttttt	ttcgctgaa	ttagctacag	atcctcctca	caagcggtea	50
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<210> 270

<211> 519

<212> DNA

<213> Homo sapien

<400> 270

tggttgcgac	caaataaccc	accagcttct	tgcacacttc	gcagaagcca	cgtccttttg	60
gctgagtcac	gtgaacgggc	agtgcgaagca	gccgcgtgcc	agagcagagg	tgcagcatgc	120
tgcacaccag	ctcagggctg	acctcctcca	gcaggatgga	caggatggag	ctgccgtacg	180
tgtccaccac	ctcctggcac	tcttcgcgaca	gggacttcgg	cagcttcgag	cacattttgt	240
caaaagcgtc	gagtatttct	ttctcagtct	tggtgtgtgc	aatcagcttg	gtcacctcct	300
tcaccaggaa	ttcacacacc	tcacagtaaa	catcagactt	tgctggggacc	tgtgtcttct	360
taatgggctc	caccagttcc	agggcaggga	tgacattctc	ggaggccact	ttggcggggga	420
ccagagtctg	catgggcate	tctttcacct	catcacagaa	cccaaccago	gcacagatct	480
ccttggggtg	catgtgcate	atcatctggg	atcgcaaca			519

<210> 271

<211> 457

<212> DNA

<213> Homo sapien

<400> 271

tttttttttt	ttcgggcggc	gaccggacgt	gcactcctcc	agtagcggt	gcacgtcgtg	60
ccaatggccc	gctatgagga	ggtgagcgtg	tccggcttcg	aggagtcca	cggggccgtg	120
gaacagcaca	atggcaagac	cattttcgcc	tactttacgg	gttctaagga	cgcggggggg	180
aaaagctggg	gccccgactg	cgtgcaggct	gaaccagtcg	tacgagaggg	gctgaagcac	240
attagtgaag	gatgtgtgtt	catctactgc	caagtaggag	aagagcctta	ttggaaagat	300
ccaaataatg	acttcagaaa	aaacttgaaa	gtaacagcag	tgctacact	acttaagtat	360
ggaacacctc	aaaaactggg	agaatctgag	tgtcttcagg	ccaacctggg	ggaaatggtg	420
ttctctgaag	attaagattt	taggatggca	atcaaga			457

<210> 272

<211> 102

<212> DNA

<213> Homo sapien

<400> 272

tttttttttt	ttgggcaaca	acctgaatac	cttttcaagg	ctctggcttg	ggctcaagcc	60
cgcgaggga	atgcaactgg	ccaggtcaca	gggcaatcaa	ga		102

<210> 273

<211> 455

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(455)

<223> n = A,T,C or G

<400> 273

tttttttttt	ttggcaatca	acagggttaa	gtcttcggcc	gaagttaatc	tcgtgttttt	60
ggcaatcaac	aggtttaagt	cttcggccga	agttaatctc	gtgttttttg	caatcaacag	120
gtttaagtct	tcggccgaag	ttaatctcgt	gtttttggca	atcaacaggt	ttaagtcttc	180
ggccgaagtt	aatctcgtgt	ttttggcaat	caacagggtt	aagtcttcgg	ccgaagttaa	240
tctcgtgttt	ttggcaatca	acagggttaa	gtcttcggcc	gaagttaatc	tcgtgttttt	300
ggcaatcaag	aggtttaagt	cttcggccga	agttaatctc	gtgttttttg	caatcaacag	360
gtttaagtct	tcggccgaan	ttaatctcgt	gtttttggca	atcaacaggt	ttaantcttc	420
ggccgaagtt	aatctcgtgt	ttttggcaat	caana			455

<210> 274

<211> 461

<212> DNA

<213> Homo sapien

<400> 274

tttttttttt	ttggccaata	cccttgatga	acatcaatgt	gaaaatcctc	ggtaaaatac	60
tggcaaacca	aatccagcag	cacatcaaaa	agcttatcca	ccatgatcaa	gtgggcttca	120
tccttgggat	gcaaggctgg	ttcaacataa	gaaaatcaat	aaatgtaatc	catcacataa	180
acagaaccaa	agacaaaaac	cacatgatta	tctcaataga	tgcagaaaag	gccttggaca	240
aattcaacag	cccttcatgc	ttaaacactct	taataaacta	gatattgatg	gaatgtatct	300
caaaataata	agagctatatt	atgacaaacc	cacagccaat	atcatactga	atgggcaaaag	360
actggaagca	ttccctttga	aaactggcac	aagacaagga	tgccctctct	caccgctcct	420
attcaacata	gtattggaag	ttctggccag	ggcaatcaag	a		461

<210> 275

<211> 729

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(729)

<223> n = A,T,C or G

<400> 275

tttttttttt	ttggccaaca	ccaagtcttc	cacgtgggag	gttttattat	gttttacaac	60
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ctccccaaac	cccaccttca	cagcctcttc	cacacgtctc	ccanagattg	ttgtccttca	180
cttgcaaat	canggatgtt	ggaagtngac	attnnagtn	gcnggaaccc	catcagtga	240
ncantaagca	gaantacgat	gactttgana	nacantgat	gaagaacacn	ctacnganaa	300
ccctttctnt	cgtgttanga	tctcnngtcc	ntcactaatg	cggccccctg	cnggtccacc	360
atttgggaga	actcccccn	cgttggatcc	ccccttgagt	ntcccattct	ngtccccan	420
accngncttg	ngngncantn	cnnccctenca	ccttggttcc	ctgnngtnaa	aatnngtttt	480
nccgccnccc	naattccac	ccnaatcaca	gcgaancng	aaggccttcn	naagtgttta	540
angcccnng	gttctctent	ntanttgca	cctaccctcc	cnettnnnnt	tnegngttg	600
tcgcgccctg	gnncgcctn	gttctctttt	nnggnnaca	cctngntcnn	nggcncntcn	660
nnctnttcc	tnnnactagc	tngectntcc	ncnccgnggn	ncanngcaca	ttncncnnac	720
tntgtnncc						729

<210> 276

<211> 339

<212> DNA

<213> Homo sapien

<400> 276

tgacctgaca	tgtagtagat	acttaataaa	tatttgtgga	atgaatggat	gaagtggagt	60
tacagagaaa	aatagaaaag	tacaaattgt	tgtcagtgtt	ttgaaggaaa	attatgatct	120
ttcccaaagt	tctgacttca	ttctaagaca	gggttagtat	ctccatacat	aattttactt	180
gcttttgaaa	atcaaagtag	ataatctatt	tagattgata	atttatttag	actggctata	240
aactattaag	tgctagcaaa	tatacatttt	aatctcattt	tccacctctt	gtgatatagc	300
tatgtaggtg	ttgactttaa	tggatgtcag	gtcaatccc			339

<210> 277

<211> 664

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(664)

<223> n = A,T,C or G

<400> 277

tgacctgaca	tccataacaa	aatctttctc	cattatatcc	ttctagggga	atttcttgaa	60
aagcatccaa	aggaaacaaa	tgatggtaag	accgtgccaa	gtggggagca	gacaccaaag	120
taagaccaca	gattttacat	tcaacaggta	gtcacagta	ctttgcccga	cactgtgggc	180
agaaatagcc	tcctaatgta	agccctggct	cagtattgcc	atccaaatgc	gccatgctga	240
aagagggttt	tgcatcctgg	tcagatnaag	aagcaatggg	gtgctgagga	aatcccatac	300
gaataagtga	gcattcagaa	cttgagctag	caggaggagg	actaagatga	tgtgtgagca	360
actctttgta	atggctttca	tctaaaataa	catggtacgt	gccaccagtt	tcacgagcaa	420
gtacagtgca	aacgcgaact	tctgcagaca	atccaataac	agatactcta	attttagctg	480
cctttagggt	cttgattaaa	tcataaatat	tagatggatc	gcaagttgta	aggntgctaa	540
aagatgatta	gtacttctcg	acttgatgtg	ccaggcatgt	tgttttaaan	tctgccttag	600
nccctgctta	ggggaatttt	taaagaagat	ggctctccat	gttcanggtc	aatcacnaat	660
tgcc						664

<210> 278

<211> 452

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(452)
 <223> n = A,T,C or G

<400> 278
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 gacacagagt gggcctctga taattcatga aatgcattct gaagtcaccc agaattggagg 120
 ctgcaatctg ctgtgctttg ggggttgcc cactgtgtct ctggatatca cacaaaagct 180
 gcaatccttc ttcttcaact aacattttgc agtattttgt gggattttta ctgcagacat 240
 gatacatagc ccatagtgcc cagagctgaa cctctggttg agagaagttg ccaaggagcg 300
 ggaaaaatgt cttgaaagat ctatagggtca ccaatgctgt catcttataa cttgaacttg 360
 gccaatctctg tatggttgca tgcagatctt ggagaagagt acgcctcttg aagtcacggg 420
 atatccaaan ctgtctgtca gatgtcaggt ca 452

<210> 279
 <211> 274
 <212> DNA
 <213> Homo sapien

<400> 279
 tttttttttt ttcggaagg caaatttact tctgcaaaaagggtgctgctt gcacttttgg 60
 ccactgagag agcacaccaa acaaagtagg yaaggggttt ttatccctaa cgcggttatt 120
 ccctgggttct gtgtcgtgtc cccattggct ggagtcagac tgcacaatct acactgaccc 180
 aactggctac tgtttaaaat tgaatatgaa taattaggtg ggaaggggga ggctgtttgt 240
 tacggtacaa gacgtgtttg ggcattgtcag gtca 274

<210> 280
 <211> 272
 <212> DNA
 <213> Homo sapien

<400> 280
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 gaaaatgaat gaactagcaa tgcgtgtatc aacatgaata aatccccaaa acataataat 120
 gttgaatgga aaagggtgagt ttcagaagga tatatatgcc ctctaaatcc atttatgtaa 180
 acctttaaaa aactacatta tttatgggtca taagtccatc cagaaaatat ttaaaaacct 240
 acatgggatt gataactact gatgtcaggt ca 272

<210> 281
 <211> 431
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(431)
 <223> n = A,T,C or G

<400> 281
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 aatttttatg ttctcttgaa taatcaaaag agtaggcaac attggttccct cattcttgaa 120
 tagcattaat cagaaaatat tgcatagcct ctagcctcct tagagtaggt gtgctctctc 180
 aaatatatca tagtcccaca gtttatttca tgtatatatt ctgcctgaat cacatagaca 240
 tttgaatttg caacgcctga tgtaaatata taaattctta ccaatcagaa acatagcaag 300
 aaattcaggg acttggtcat yatcagggtg tgacagcana tccctgtara aacactgata 360

cacactcaca cacgtatgca acgtggagat gtcgcyttww kkktywycwm rmrycrwecn 420
aatcacttan n 431

<210> 282
<211> 98
<212> DNA
<213> Homo sapien

<400> 282
attcgattcg atgcttgagc ccaggagttc aagactgcag tgagccactg cacttcaggc 60
tggacaacag agcgagtccc tgtgcaaaa aaaaaaaa 98

<210> 283
<211> 764
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (764)
<223> n = A,T,C or G

<400> 283
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tataaactgc tgtatctagg ggcaggacca agggggcagg ggcaacagcc ccagcgtgca 120
ggggccascac tgcacagtgg astgcaaagg ttgcaggcta tgggcggcta ctavtaaccc 180
cgtttttccct gtattatctg taacataata tggtagactg tcacagagcc gaatwccart 240
hacasgatga atccaawggt caygaggatg cccasaatca gggcccasat sttcaggcac 300
ttggcggtgg gggcatasgc ctgkgccccg gtcacgtcsc caaccwtcty cctgtcccta 360
cmcttgawtc cncnccttnn nntncctna tntgcccgc cncctcctng ngteaaccng 420
natctgcact anctccctcn ccccttntgg antctcntcc ttcaantaan nttatccttn 480
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cncntnctn cnnatcggtc cncctnntaa ctacnctttn naannncct cactnatncc 600
ngnnantttct ttccttccct ccnagcgnn tgcgtgcgcc cgtctngcct nnnctncgna 660
cccnactttt atttaccttt ncaccctagc nctctacttn acccancnc tectacctcc 720
nggnccaccc nncctnatc nctnctctn tennctcntt cccc 764

<210> 284
<211> 157
<212> DNA
<213> Homo sapien

<400> 284
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atttctcccc ttccaggaaac gtcttgcag gatgatcaaa gatcagctcc tgggtcaacat 120
aaataagcta gtttaagata cgttcccccta cacttga 157

<210> 285
<211> 150
<212> DNA
<213> Homo sapien

<400> 285
attcgattgt actcagacaa caatatgcta agtgggaagaa gtcagtcaca aaagaccaca 60
tactgtatga cttcatttac attaagtgtc cagaataggc aaatccgtag agacagaaag 120

tagatgagca gctgcctagg tctgagtaca

150

<210> 286

<211> 219

<212> DNA

<213> Homo sapien

<400> 286

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ataaatgcaa gtctcaccac cagatgtgaa attacagtaa actttgaagg aatctcctga	120
gcaaccttgg ttaggatcaa tccaatattc accatctggg aagtcaggat ggctgagttg	180
caggtcttta caagttcggg ctggattggg ctgagtaca	219

<210> 287

<211> 196

<212> DNA

<213> Homo sapien

<400> 287

attcgattct tgaggctacc aggagctagg agaagaggca tggaacaaat tttccctcat	60
atccatactc agaaggaacc aacctgctg acaccttaat ttcagcttct ggcctctaga	120
actgtgagag agtacatttc tcttggttta agccaagaga atctgtcttt tgggtacttta	180
tatcatagcc tcaaga	196

<210> 288

<211> 199

<212> DNA

<213> Homo sapien

<400> 288

attcgatttc agtccagtc cagaaccac attgtcaatt actactctgt araagattca	60
tttgttgaaa ttcattgagt aaaacattta tgatccctta atatatgcca attaccatgc	120
taggtactga agattcaagt gaccgagatg ctagcccttg ggttcaagtg atccctctcc	180
cagagtgcac tggactgaa	199

<210> 289

<211> 182

<212> DNA

<213> Homo sapien

<400> 289

attcgattct tgaggctaca aacctgtaca gtatgttact ctactgaata ctgtaggcaa	60
tagtaataca gaagcaagta tctgtatatg taaacattaa aaaggtacag tgaaacttca	120
gtattataat cttagggacc accattatat atgtgggtcca tcattggcca aaaaaaaaaa	180
aa	182

<210> 290

<211> 1646

<212> DNA

<213> Homo sapien

<400> 290

ggcacgagga gaaatgtaat tccatatttt atttgaaact tattccatat ttttaattgga	60
tattgagtga ttgggttatc aaacaccac aaactttaat tttgttaaat ttatatggct	120
ttgaaataga agtataagtt gctaccattt ttgataaca ttgaaagata gtattttacc	180

atctttaatc	atcttgga	atacaagtc	tgtgaacaac	cactctttca	cctagcagca	240
tgaggccaaa	agtaaaggct	ttaaattata	acatatggga	ttcttagtag	tatgtttttt	300
tcttgaaact	cagtggctct	atctaaccct	actatctcct	cactctttct	ctaagactaa	360
actctagget	cttaaaaaatc	tgcccacacc	aatcttagaa	gctctgaaaa	gaatttgtct	420
ttaaatatct	tttaatatga	acatgtatct	tatggacca	attgacattt	tcgactatct	480
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gcagtctcct	ttaaggtaga	acaaatactt	tctatctttt	tttcaccatt	gtgggattgg	660
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gagcagaagc	aaaccacatg	tctcagctat	attattatct	attttttatg	cataaagtga	1020
atcatttctt	ctgtattaat	ttccaaaggg	ttttaccctc	tatttaaatg	ctttgaaaaa	1080
cagtgcattg	acaatgggtt	gatatttttc	tttaaaagaa	aaatataatt	atgaaagcca	1140
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ctggtaattt	ttttattttac	aatatgttta	aagagataac	agtttgatat	gttttcatgt	1440
gtttatagca	gaagttatct	atttctatgg	cattccagcg	gatatttttg	tggttgcgag	1500
gcatgcagtc	aatattttgt	acagttatgt	gacagtattc	agcaacgcct	gatagcttct	1560
ttggccttat	gttaaaataaa	aagacctgtt	tgggatgtat	tttttatttt	taaaaaaaaa	1620
aaaaaaaaaa	aaaaaaaaaa	aaaaaa				1646

<210> 291

<211> 1851

<212> DNA

<213> Homo sapien

<400> 291

tcatacccat	tgccagcagc	ggcacggtta	gtcagggtttt	ctgggaatcc	cacatgagta	60
cttccgtgtt	cttcattctt	cttcaatagc	cataaatctt	ctagctctgg	ctggctgttt	120
tcacttcctt	taagcctttg	tgactcttcc	tctgatgtca	gctttaagtc	ttgttctgga	180
ttgctgtttt	cagaagagat	ttttaacatc	tgtttttctt	tgtagtcaga	aagtaactgg	240
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cagcaagtat	gagagcagtt	cttccatata	tatccagcgc	atttaaattc	gcttttttct	420
tgattaaaaa	tttcaccact	tgtctgtttt	gctcatgtat	accaagtagc	agtgggtgtga	480
ggccatgctt	gttttttgat	tccatatacag	caccgtataa	gagcagtgct	ttggccatta	540
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ttggatcagt	gccatgttcc	agcaacatta	acgcacatcc	atcttctctg	cattgtacgg	660
cctttgtcag	agctgtcttc	tttttgttgt	caaggacatt	aagtgtgacat	cgtctgtcca	720
gcacgagttt	tactacttct	gaattcccat	tggcagaggg	cagatgtaga	gcagtcctct	780
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ggacttttacc	ccaccaggca	gctctgtgga	gcttgtccag	atcttctcca	tggacgtggt	900
acctggggtc	catgaaggcg	ctgtcatcgt	agtctcccca	agcgaccacg	ttgctcttgc	960
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gtccatccag	ggaggaagaa	atgcaggaaa	tgaaagatgc	atgcacgatg	gtatactcct	1140
cagccatcaa	acttctggac	agcaggtcac	ttccagcaag	gtggagaaag	ctgtccaccc	1200
acagaggatg	agatccagaa	accacaatat	ccattcacaa	acaaacactt	ttcagccaga	1260
cacaggtact	gaaatcatgt	catctgcggc	aacatgggtg	aacctaccca	atcacacatc	1320
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<210> 292
<211> 1851
<212> DNA
<213> Homo sapien

<400> 292						
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cttccgtggt	cttcattctt	cttcaatagc	cataaatctt	ctagctctgg	ctggctgttt	120
tcacttcctt	taagcctttg	tgactcttcc	tctgatgtca	gctttaagtc	ttgttctgga	180
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caaattacat	gatgatgact	agaaacagca	tactctctgg	ccgtctttcc	agatcttgag	300
aagatacatc	aacattttgc	tcaagtagag	ggctgactat	acttgctgat	ccacaacata	360
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tgattaaaaa	tttcaccact	tgctgttttt	gtcatgtat	accaagtagc	agtggtgtga	480
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cagccatcaa	acttctggac	agcagggtcac	ttccagcaag	gtggagaaaag	ctgtccaccc	1200
acagaggatg	agatccagaa	accacaatat	ccattcaca	acaaacactt	ttcagccaga	1260
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<210> 293
<211> 668
<212> DNA
<213> Homo sapien

<400> 293						
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accrtataag	agcagtgcct	tggccattaa	tttatcttct	atrttagaca	gcrtagtgya	180
gagtggatt	tccatactca	tctggaatat	ttggatcagt	gccaatgttc	agcaacatta	240
acgcacattc	atcttccctg	cattgtacgg	cctgtcagta	ttagacccaa	aaacaaatta	300
catatcttag	gaattcaaaa	taacattcca	cagctttcac	caactagtta	tattttaaagg	360
agaaaactca	tttttatgcc	atgtattgaa	atcaaaccce	cctcatgctg	atatagtgtg	420
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cgtctgtcca	gcaggagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	540
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aaaaaaaa						668

<210> 294
 <211> 1512
 <212> DNA
 <213> Homo sapien

<400> 294						
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<210> 295
 <211> 1853
 <212> DNA
 <213> Homo sapien

<400> 295						
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<210> 296

<211> 2184

<212> DNA

<213> Homo sapien

<400> 296

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<210> 297

<211> 1855

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (1855)

<223> n = A,T,C or G

<400> 297

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<210> 298
 <211> 1059
 <212> DNA
 <213> Homo sapien

<400> 298						
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<210> 299
 <211> 329
 <212> PRT
 <213> Homo sapien

<400> 299																	
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			20					25					30				
Glu	Tyr	Thr	Ile	Val	His	Ala	Ser	Phe	Ile	Ser	Cys	Ile	Ser	Ser	Ser		
		35					40					45					
Leu	Asp	Gly	Gln	Gly	Glu	Arg	Gln	Glu	Gln	Arg	Gly	His	Phe	Trp	Arg		
	50					55			60								
Pro	Gln	Arg	Leu	Leu	Cys	Glu	Asp	Ala	Trp	Glu	Gln	Glu	Val	Gln	Val		
65					70				75					80			
Val	Leu	Pro	Leu	Leu	Pro	Leu	Leu	Gln	Gly	Ser	Gly	Lys	Ser	Asn	Val		
			85					90						95			
Val	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe	Met	Asp	Pro	Arg	Tyr		
		100						105					110				
His	Val	His	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His	Arg	Ala	Ala	Trp	Trp		
		115					120					125					
Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met	Leu	Arg	Asp	Thr	Asp		
	130					135					140						
Val	Asn	Lys	Arg	Asp	Lys	Gln	Lys	Arg	Thr	Ala	Leu	His	Leu	Ala	Ser		

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145          150          155          160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
          165          170          175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
          180          185          190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
          195          200          205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
          210          215          220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
          225          230          235          240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
          245          250          255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
          260          265          270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
          275          280          285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu
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Ser Met Leu Phe Leu Val Ile Ile Met
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<210> 300

<211> 148

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(148)

<223> Xaa = Any Amino Acid

<400> 300

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Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys
          35          40          45
Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
          50          55          60
Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
          65          70          75          80
Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
          85          90          95
Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
          100          105          110
Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
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Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser
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Lys Asn Lys Val
145

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<210> 301
 <211> 1155
 <212> DNA
 <213> Homo sapien

<400> 301

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gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	ttctgactac	1080
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accagaaata	aataa					1155

<210> 302
 <211> 2000
 <212> DNA
 <213> Homo sapien

<400> 302

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accactctgc	actacgctat	ctataatgaa	gataaattaa	tggccaaagc	actgctctta	780
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catgagcaaa	aacagcaagt	cgtgaaat	ttaatcaaga	aaaaagcgaa	tttaaatgca	900
ctggatagat	atggaaggac	tgctctcata	cttgcgtgat	gttgtggatc	agcaagtata	960
gtcagccttc	tacttgagca	aaatattgat	gtatcttctc	aagatctatc	tggacagacg	1020
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aaaaaaaaaa	aaaaaaaaaa					2000

<210> 303

<211> 2040

<212> DNA

<213> Homo sapien

<400> 303

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gaaaaagaca	tcttgcatga	aaatagtacg	ttgcgggaag	aaattgccat	gctaagactg	1980
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<210> 304
 <211> 384
 <212> PRT
 <213> Homo sapien

<400> 304
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 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys
 370 375 380

<210> 305
 <211> 656
 <212> PRT
 <213> Homo sapien

<400> 305
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
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 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys


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385          390          395          400
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
          405          410          415
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
          420          425          430
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
          435          440          445
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
          450          455          460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
465          470          475          480
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
          485          490          495
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
          500          505          510
Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys
          515          520          525
Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly
          530          535          540
Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser
545          550          555          560
Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr
          565          570          575
His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln
          580          585          590
Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln
          595          600          605
Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys
610          615          620
Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile
625          630          635          640
Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
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<210> 306
<211> 671
<212> PRT
<213> Homo sapien

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<400> 306
Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
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Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
20          25          30
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
35          40          45
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
50          55          60
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
65          70          75          80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
85          90          95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
100          105          110
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe

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115	120	125
Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His		
130	135	140
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met		
145	150	155
Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala		
165	170	175
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu		
180	185	190
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr		
195	200	205
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met		
210	215	220
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn		
225	230	235
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys		
245	250	255
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly		
260	265	270
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val		
275	280	285
Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr		
290	295	300
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile		
305	310	315
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu		
325	330	335
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val		
340	345	350
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile		
355	360	365
Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu		
370	375	380
Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys		
385	390	395
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu		
405	410	415
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn		
420	425	430
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro		
435	440	445
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu		
450	455	460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu		
465	470	475
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp		
485	490	495
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu		
500	505	510
Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp		
515	520	525
Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys		
530	535	540
His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala		
545	550	555
		560

Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg
 565 570 575
 Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His
 580 585 590
 Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn
 595 600 605
 Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile
 610 615 620
 Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys
 625 630 635 640
 Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala
 645 650 655
 Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
 660 665 670

<210> 307
 <211> 800
 <212> DNA
 <213> Homo sapien

<400> 307
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 acttcatttt tggtagataa catctttata ggacaggggt aaaatcccaa tactaacagg 120
 agaatgctta ggactctaac aggtttttga gaatgtgttg gtaagggcca ctcaatccaa 180
 tttttcttgg tccctccttg ggtctaggag gacaggcaag ggtgcagatt ttcaagaatg 240
 catcagtaag ggccactaaa tccgaccttc ctctgttctc cttgtggtct gggaggaaaa 300
 ctagtgtttc tggtgctgtg tcagttagca caactattcc gatcagcagg gtccagggac 360
 cactgcagggt tcttgggcag ggggagaaac aaaacaaacc aaaaccatgg gcrgttttgt 420
 ctttcagatg ggaaacactc aggcatacaac aggtcacct ttgaaatgca tccaaagcca 480
 atgggacaaa tttgacctac aaaccctgga aaaagaggtg gtcattttt tttgcactat 540
 ggcttgcccc caacattctc tctctgatgg ggaaaaatgg ccacctgagg gaagtacaga 600
 ttacaatact atcctgcagc ttgacctttt ctgtaagagg gaaggcaaatt ggagtgaat 660
 accttatgtc caagctttct tttcattgaa ggagaatata ctatgcaaag cttgaaattt 720
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<210> 308
 <211> 102
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(102)
 <223> Xaa = Any Amino Acid

<400> 308
 Met Gly Xaa Phe Val Phe Gln Met Gly Asn Thr Gln Ala Ser Thr Gly
 1 5 10 15
 Ser Pro Leu Lys Cys Ile Leu Ser Gln Trp Asp Lys Phe Asp Pro Gln
 20 25 30
 Thr Leu Glu Lys Glu Val Ala His Phe Phe Cys Thr Met Ala Trp Pro
 35 40 45
 Gln His Ser Leu Ser Asp Gly Glu Lys Trp Pro Pro Glu Gly Ser Thr
 50 55 60

Asp Tyr Asn Thr Ile Leu Gln Leu Asp Leu Phe Cys Lys Arg Glu Gly
 65 70 75 80
 Lys Trp Ser Glu Ile Pro Tyr Val Gln Ala Phe Phe Ser Leu Lys Glu
 85 90 95
 Asn Thr Leu Cys Lys Ala
 100

<210> 309
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 309
 Leu Met Ala Glu Glu Tyr Thr Ile Val
 1 5

<210> 310
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 310
 Lys Leu Met Ala Lys Ala Leu Leu Leu
 1 5

<210> 311
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 311
 Gly Leu Thr Pro Leu Leu Gly Ile
 1 5

<210> 312
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 312
 Lys Leu Val Leu Asp Arg Arg Cys Gln Leu
 1 5 10

<210> 313
<211> 1852
<212> DNA
<213> Homo sapiens

<400> 313
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aaaaccacct atgacaagcc cacagccaac ataatactaa atggggaaaa gttagaagca 120
tttctctga gaactgcaac aataaatata aggatgctgg attttgtcaa atgccttttc 180
tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240
ttattgactt gctgtgtta gaccggaaga gctgggggtg ttctcaggag ccaccgtgtg 300
ctgcggcagc ttccgggataa cttgaggctg catcactggg gaagaaacac aytccgtgcc 360
gtggcgctga tggctgagga cagagcttca gtgtggcttc tctgcgactg gcttcttcgg 420
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tggatgaaga gtattacgtt gtgcagatat actgcagtgt cttcatctct tgatgtgtga 540
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ccatcgtgca tgcactcttc atttcttgca tttcttctc cctggatgga cagggggagc 780
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tttctgacta caaagaaaaa cagatgttaa aaatctctc tgaaaaacagc aatccagaac 1680
aagacttaaa gctgacatca gaggaagagt cacaagggt taaagggaagt gaaaacagcc 1740
agccagagct agaagattta tggctattga agaagaatga agaacacgga agtactcatg 1800
tgggattccc agaaaacctg actaacgggt cgcgtgctgg caatggtgat ga 1852

<210> 314
<211> 879
<212> DNA
<213> Homo sapiens

<400> 314
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cttaatgtcc ttgacaacaa aaagaggaca gctctgacaa aggccgtaca atgccaggaa 480
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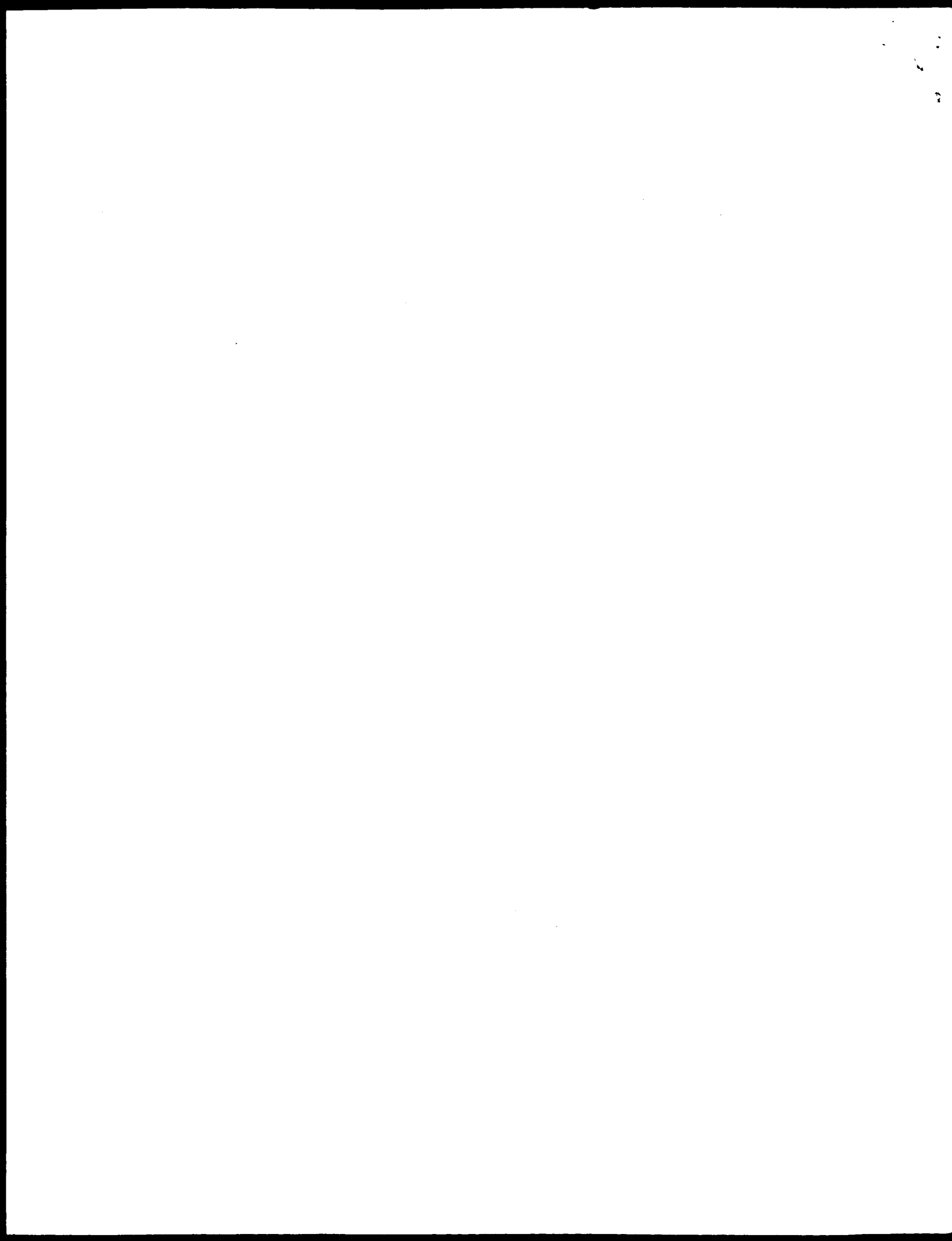
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ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ,
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For two-letter codes and other abbreviations, refer to the "Guid-
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ning of each regular issue of the PCT Gazette.

(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER



cDNA PREPARED FROM
NORMAL BREAST TISSUE
FROM THE SAME PATIENT

cDNA PREPARED
FROM BREAST TUMOR

WO 00/61753 A3

(57) Abstract: Compositions and methods for the detection and therapy of breast cancer are disclosed. The compounds provided include nucleotide sequences that are preferentially expressed in breast tumor tissue, as well as polypeptides encoded by such nucleotide sequences. Vaccines and pharmaceutical compositions comprising such compounds are also provided and may be used, for example, for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of antibodies, which are useful for diagnosing and monitoring the progression of breast cancer in a patient.

INTERNATIONAL SEARCH REPORT

Int. Application No.
PCT/US 00/09312

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/47 C07K16/18 C07K19/00 C12N15/62
A61K38/17 A61K39/395 A61K48/00 C12N5/08 G01N33/574
C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K A61K G01N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EP0-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 45328 A (CORIXA CORPORATION) 15 October 1998 (1998-10-15) page 2, line 7 -page 5, line 22 page 7, line 23 -page 24, line 11; examples 1-4 sequence listing SEQ ID NOs:1, 3-10, 227 ---	1,2,4-60
X	WO 97 25426 A (CORIXA CORPORATION) 17 July 1997 (1997-07-17) page 2, line 8 -page 5, line 11 page 7, line 14 -page 23, line 2; example 1 sequence listing SEQ ID NO:1, 3-10, 227 --- -/--	1,2,4-60

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

8 August 2000

Date of mailing of the international search report

08. 11. 00

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MONTERO LOPEZ B.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/09312

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>WO 97 25431 A (CORIXA CORPORATION) 17 July 1997 (1997-07-17) page 2, line 3 -page 3, line 25 page 4, line 12 -page 17, line 18; examples 1-4 sequence listing SEQ ID NOs:1, 3-10 -----</p>	1,2,4-10

INTERNATIONAL SEARCH REPORT

international application No.
PCT/US 00/09312

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely.

Although claims 21, 22, 29-31 34 37-39 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1, 2, 4-60 Partially.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Partially 1, 2, 4-60

Breast cancer related polypeptide B18Ag1, corresponding polynucleotides comprising SEQ ID NOs:1, 3-10, or 227, and derived oligonucleotides; variants thereof, expression vector and host cell comprising the same; antibody and diagnostic kit containing it, fusion protein comprising the polypeptide; pharmaceutical composition and vaccine comprising any of the above and use therefor in the treatment of cancer, and for removing tumor cells from a sample; use of the polypeptides for stimulating and expanding T-cells and use of such T-cells for inhibiting cancer development; use of the polypeptides for determining the presence of cancer or monitoring the progression of cancer in a patient.

2. Claims: Partially 1-60

Idem as subject 1 for Breast cancer related polypeptide and polynucleotide B21GT2 (B311D) comprising SEQ ID NOs:56, 307, 308, 316 or 317.

3. Claims: Partially 1, 2, 4-60

Idem as subject 1 for Breast cancer related polypeptide and polynucleotide B15Ag1 comprising SEQ ID NOs:27 or 290.

4. Claims: Partially 1, 2, 4-60

Idem as subject 1 for Breast cancer related polypeptide and polynucleotide B31GA1b comprising SEQ ID NOs:148.

5. Claims: Partially 1, 2, 4-60

Idem as subject 1 for Breast cancer related polypeptide and polynucleotide B38GA2a comprising SEQ ID NOs:157.

6. Claims: Partially 1-60

Idem as subject 1 for Breast cancer related polypeptide and polynucleotide B11Ag1 (B305D) and its isoform A comprising SEQ ID NO:292-306, or 309-315.

7. Claims: Claims: Partially 1, 2, 4-60,
all as far as applicable

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Breast cancer related polypeptides, corresponding polynucleotides comprising SEQ ID NOs:11-26 (inventions 7-22), 28-55 (inventions 23-50), 57-86 (inventions 51-80), 142-147 (inventions 81-86), 149-156 (inventions 87-94), 158-226 (inventions 95-163), 228-253 (inventions 164-189), or 255-291 (inventions 190-226), and derived oligonucleotides; variants thereof, expression vector and host cell comprising the same; antibody and diagnostic kit containing it, fusion protein comprising the polypeptide; pharmaceutical composition and vaccine comprising any of the above and use therefor in the treatment of cancer, and for removing tumor cells from a sample; use of the polypeptides for stimulating and expanding T-cells and use of such T-cells for inhibiting cancer development; use of the polypeptides for inhibiting or monitoring the progression of cancer in a patient, as far as applicable.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Int. Application No

PCT/US 00/09312

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9845328 A	15-10-1998	AU 6956098 A EP 0975666 A NO 994932 A PL 336349 A ZA 9802968 A	30-10-1998 02-02-2000 07-12-1999 19-06-2000 27-10-1998
WO 9725426 A	17-07-1997	AU 1697497 A BR 9707125 A CA 2242340 A CN 1211279 A EP 0874902 A NO 983183 A	01-08-1997 20-07-1999 17-07-1997 17-03-1999 04-11-1998 10-09-1998
WO 9725431 A	17-07-1997	AU 1575697 A	01-08-1997

